

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 19:55:00 ; Search time 408 Seconds
(without alignments)
8496.396 Million cell updates/sec

Title: US-10-089-557-2_COPY_1_816
Perfect score: 816
Sequence: 1 actataggcagcgcgtgctc.....tatttcagtattgttaaag 816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	3041	6 AAS19999	Aas19999 Cotton CF
2	124.6	15.3	8056	7 ABZ10246	Abz10246 Haematopo
3	123	15.1	8056	7 ABZ10100	Abz10100 Haematopo
C 4	103.2	12.6	8056	7 ABZ10246	Abz10246 Haematopo
C 5	97.8	12.0	8056	7 ABZ10100	Abz10100 Haematopo
C 6	97	11.9	8310	2 AAZ29911	Aaz29911 CDNA enco
7	94.2	11.5	494	5 ABV10021	Abv10021 Human pro
8	90.2	11.1	7351	6 ABL32029	Ab132029 Human imm
9	90.2	11.1	8305	6 ABL33569	Ab133569 Human imm
10	89.8	11.0	18357	6 ABQ67084	Abq67084 Human ang
11	89.4	11.0	6106	4 AAS46429	Aas46429 Tumour su
12	89.4	11.0	6106	6 ABK40031	Abk40031 Human che
13	89.4	11.0	6106	6 ABL33472	Ab133472 Human imm
14	89	10.9	6478	9 ADB54284	Adb54284 Pretreate
15	88.2	10.8	16602	6 ABL32727	Ab132727 Human imm
16	88.2	10.8	16602	6 ABN80069	Abn80069 Human che
17	88	10.8	5852	2 AAQ11710	Aaq11710 Dictyoste
18	87.8	10.8	419	7 ABX46069	Abx46069 Bovine ES
19	87.4	10.7	17848	4 AAS45323	Aas45323 Chemical1
20	87.4	10.7	17848	6 ABK39976	Abk39976 Human che
21	87.4	10.7	17848	6 ABK28164	Abk28164 DNA trans
22	87.2	10.7	15548	6 ABL34155	Ab134155 Human imm
23	86.6	10.6	1501	7 ABZ10188	Abz10188 Haematopo

24	86.6	10.6	1501	9 ADE84162	Adé84162 Human lym
C 25	86	10.5	29993	9 ADB37661	Adb37661 Human che
C 26	86	10.5	38342	4 AAS46746	Aas46746 Tumour su
C 27	86	10.5	38342	6 ABK31507	Abk31507 Signal tr
28	85.8	10.5	5487	6 ABL33598	Ab133598 Human imm
29	85.8	10.5	7508	6 ABK31207	Abk31207 Signal tr
30	85.4	10.5	3051	7 ACE62818	Acf62818 Colon can
31	85.4	10.5	5952	9 ADB54320	Adb54320 Pretreate
32	85.2	10.4	6465	6 ABL32985	Ab132985 Human imm
C 33	85.2	10.4	9789	2 AAT41852	Aat41852 CDNA enco
C 34	84.8	10.4	1671	2 AAQ24134	Aaq24134 50 KD sub
C 35	84.8	10.4	5845	6 ABL33663	Ab133663 Human imm
36	84.6	10.4	34548	6 ABL70604	Ab170604 Chemical1
37	84.4	10.3	6063	4 AAS46337	Aas46337 Tumour su
38	84.4	10.3	6216	6 ABK39932	Abk39932 Human che
39	84.4	10.3	6216	6 ABL70139	Ab170139 Chemical1
40	84.4	10.3	13511	6 ABL32281	Ab132281 Human imm
41	84.4	10.3	34548	6 ABL70603	Ab170603 Chemical1
42	84.2	10.3	6478	4 AAS45417	Aas45417 Chemical1
43	84.2	10.3	6478	6 ABK28270	Abk28270 DNA trans
44	84.2	10.3	6478	6 ABN80201	Abn80201 Human che
45	84.2	10.3	6478	9 ADB54156	Adb54156 Pretreate

ALIGNMENTS

RESULT 1
AAS19999
ID AAS19999 standard; DNA; 3041 BP.
XX AC AAS19999;
XX AC
XX AC
DT 21-MAY-2002 (first entry)
XX DT
XX DE Cotton CFACT1 gene sequence.
XX DE
KW Cotton; fibre-specific actin gene; CFACT1; improved cotton fibre;
KW high fibre quality; cotton yield; transgenic; plant; anthocyanin;
KW coloured cotton; silk protein; silk worm; spider; polyhydroxybutyrate;
KW improved thermal property; insulating characteristic; gene; ds.
XX KW
XX OS Gossypium hirsutum.
XX OS
XX PN WO200210413-A1.
XX PN
XX PD 07-FEB-2002.
XX PD
PF 01-AUG-2000; 2000WO-SG000112.
XX PF
XX PR 01-AUG-2000; 2000WO-SG000112.
XX PR
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX PA
PI Li X, Cai L, Cheng N, Liu J;
XX PI
XX DR WPI; 2002-217123/27.
XX DR
XX PT New fiber-specific actin promoter from cotton for controlling gene
PT expression in cotton fibers and creating transgenic plants, in particular
PT cotton plants, having altered fiber characteristics.
XX PT
XX PS Claim 2; Fig 2; 36pp; English.
XX PS
CC The present invention relates to the isolation of the cotton fibre-
CC specific actin gene, CFACT1, which includes the promoter sequence. The
CC cotton CFACT1 gene promoter controls specific gene expression at the
CC transcriptional level in cotton fibres. It is useful for improving cotton
CC fibres to create new cotton varieties with high fibre quality and yield,
CC by gene manipulation methodologies. The promoter is also useful for
CC creating transgenic plants, particularly cotton, having altered fibre
CC characteristics, and permits selective expression of a transgene in the
CC cotton fibre, permitting greater latitude in the types of transgenes

CC employed. Examples of expression of desirable genes in cotton fibres, but
CC not in other parts of the cotton plants, include anthocyanin genes for
CC coloured cotton, silk protein genes from silk worm or spiders for
CC increased strength cotton fibres, and biosynthesis of polyhydroxybutyrate
CC in cotton fibres for improved thermal properties and insulating
CC characteristics. The present sequence represents the cotton CFACT1 gene
XX

SQ Sequence 3041 BP; 892 A; 517 C; 629 G; 1003 T; 0 U; 0 Other;

Query Match 100.0%; Score 816; DB 6; Length 3041;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTATAGGCGCACGCGTGTGACGCGCGCGGTGTCCTCTAAGAACATTTGTCAAG 60
|||
Db 1 ACTATAGGCGCACGCGTGTGACGCGCGCGGTGTCCTCTAAGAACATTTGTCAAG 60
1 ACTATAGGCGCACGCGTGTGACGCGCGCGGTGTCCTCTAAGAACATTTGTCAAG 60
QY 61 TCGTCTTGGCCGACGAATCCGAATAGAGCTTAGAGTAACATCTAACAGCGGACTGCT 120
|||
Db 61 TCGTCTTGGCCGACGAATCCGAATAGAGCTTAGAGTAACATCTAACAGCGGACTGCT 120
QY 121 CCAGCATTAAGTGTGTTGTAAGATGTAATGTAGTGTATGCTAGTCGAAGTATTTTCAGG 180
|||
Db 121 CCAGCATTAAGTGTGTTGTAAGATGTAATGTAGTGTATGCTAGTCGAAGTATTTTCAGG 180
QY 181 AAGGTGTTAAGAAATTAATGTTATGGAGTTACTAATTTCTAGTATTAATTTGTTGGA 240
|||
Db 181 AAGGTGTTAAGAAATTAATGTTATGGAGTTACTAATTTCTAGTATTAATTTGTTGGA 240
QY 241 AGTTAATATATATTAATTAATCAATCTGTTTATTTTATTTTATTAACACATTTACAA 300
|||
Db 241 AGTTAATATATATTAATTAATCAATCTGTTTATTTTATTTTATTAACACATTTACAA 300
QY 301 TAAATTAATTAACCTTGCTGTTTTCATTTATGACCGGTAATATTTTAAATTAAT 360
|||
Db 301 TAAATTAATTAACCTTGCTGTTTTCATTTATGACCGGTAATATTTTAAATTAAT 360
QY 361 GAGCATTTATATATTAATTAATTAATCATTTGTAATATATGTAATAATTTAAAT 420
|||
Db 361 GAGCATTTATATATTAATTAATTAATCATTTGTAATATATGTAATAATTTAAAT 420
QY 421 AATAATTTATTAATATATATTAATACTCAATCAAAACAATAAAGATAATTAATTTCTA 480
|||
Db 421 AATAATTTATTAATATATATTAATACTCAATCAAAACAATAAAGATAATTAATTTCTA 480
QY 481 AATATATAAATTTTAAATAAGCTTTTCAGTAAATCTGCAAAACAATAGAAAATATTTT 540
|||
Db 481 AATATATAAATTTTAAATAAGCTTTTCAGTAAATCTGCAAAACAATAGAAAATATTTT 540
QY 541 TTGCAGGTTTCATCCAAACACAGAAAAGTAATCATTTTCAGAAAAGTAATCATTTTTC 600
|||
Db 541 TTGCAGGTTTCATCCAAACACAGAAAAGTAATCATTTTCAGAAAAGTAATCATTTTTC 600
QY 601 AGAAATTAATTTTCGGAATTAATTTTACTGCGCAACAAATGAGAGTCTAAGTGTCTGTT 660
|||
Db 601 AGAAATTAATTTTCGGAATTAATTTTACTGCGCAACAAATGAGAGTCTAAGTGTCTGTT 660
QY 661 TTTATTTTATTTTCTAATTTAGAGAAACTAGAAATGATTTGTCAAAATGCTTTAATC 720
|||
Db 661 TTTATTTTATTTTCTAATTTAGAGAAACTAGAAATGATTTGTCAAAATGCTTTAATC 720
QY 721 TAGCTGTTTAGATTAGTTGAAGGGCACAGAACCCGCTGTCAAGTATTTGCTGTAC 780
|||
Db 721 TAGCTGTTTAGATTAGTTGAAGGGCACAGAACCCGCTGTCAAGTATTTGCTGTAC 780
QY 781 TCACCTACCTAGATCTTAATTTCAAGTATTTGTAAG 816
|||
Db 781 TCACCTACCTAGATCTTAATTTCAAGTATTTGTAAG 816

RESULT 2
ABZ10246
ID ABZ10246 standard; DNA; 8056 BP.

XX
AC ABZ10246;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller U;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 386; 117bp; English.
XX

CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match 15.3%; Score 124.6; DB 7; Length 8056;
Best Local Similarity 53.3%; Pred. No. 3.9e-07;
Matches 285; Conservative 0; Mismatches 249; Indels 1; Gaps 1;

QY 189 AAGAATTAATGTTATGGGATTAATTAATTTCTAGTATTAATTTGTGTTGGAGTTAATA 248
|||
Db 1646 AAAAATTAATTTAATTAATGATTAATTAATTTTAAATTAATAAATAATTAAT 1705
QY 249 TATAATTAATCAATCTGTTTATTTTATTTTATTAACACAATTAACAATTAAT 308
|||
Db 1706 TAAATTAATTAATTAATTAATTAATTTTAAATTAATAAATAAATAATTTT 1765

[illegible]

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RESULT 3
ABZ10100
ID ABZ10100 standard; DNA; 8056 BP.
XX
AC ABZ10100;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 240; 117bp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,

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CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match	15.1%	Score 123;	DB 7;	Length 8056;
Best Local Similarity	53.1%;	Pred. No. 6.1e-07;		
Matches 284; Conservative	0;	Mismatches 250;	Indels 1;	Gaps 1;

[illegible]

RESULT 4	
ABZ10246/c	
ID	ABZ10246 standard; DNA; 8056 BP.
XX	
AC	ABZ10246;
XX	
DT	16-JAN-2003 (first entry)
XX	
DE	Haematopoietic cell proliferation disorder related DNA sequence #386.
XX	
KW	Human; haematopoietic cell proliferation disorder; cytostatic;
KW	gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW	

KW cytosine methylation state; gene; ds.
XX Homo sapiens.
OS WO200277272-A2.
XX 03-OCT-2002.
XX 26-MAR-2002; 2002WO-EP003401.
XX 26-MAR-2001; 2001US-0278333P.
XX (EPIG-) EPIGENOMICS AG.
XX PA Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX WPI; 2003-018942/01.
XX DR
XX PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX PS Claim 28; SEQ ID NO 386; 117bp; English.
XX CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
Query Match 12.6%; Score 103.2; DB 7; Length 8056;
Best Local Similarity 51.4%; Pred. No. 0.00015;
Matches 289; Conservative 0; Mismatches 268; Indels 5; Gaps 2;
QY 170 TATTTTCATGGAAGTGTTAAGAATTAATGTTATGGATTAATAATTTCTAGTAAAT 229
DB 2644 TTTTATTTATTTTAAATTAATTAATTAATTAATTTTTCATTAATTTT 2585
QY 230 TGTGTTTGAAGTAAATATAATTAATCAATCCCTGTTTATTTTATTTTAAAC 289
DB 2584 TATTTTAAATAATTTAATTAATAATTTTAAATTTTAAATTTAATTTAAATTT 2525
QY 290 ACAATTACAATAATTAATTTAACTTTGGTTGTTTCAATTTATGACGGTTAATTTTA 349
DB 2524 ATTTTATTTTCAATTAATTAATTTAATTTAATAAACAATAATAATAATAATA 2465
QY 350 GTTTAATAATTGAGCATTAATATATATTAATAATAATCAATGTAATATATGTAATAA 409
DB 2464 TAAATAAAAAATAAAAAATAATTAATTTTAAAAATAATAATTAATTTTAAATTT 2405
QY 410 TAAATTAATAATAATAATTTAATTAATATATATAATAAATCAATCAACAATAAAAAAGATA 469

DB 2404 TCAAAAAATATAATAATTTAATAATTTATTTAATAAAAAATAAAAAATTAATTTAAAAATTT 2345
QY 470 ATAAATTTCTTAATATAATAATTTTAAATATAGCTTTTCAGTAAATCTGTCAACATA 529
DB 2344 AAATAAAATTTAATTAATAACAATAATTAATAATTAATTTTAAAAATAATAATAATAA 2285
QY 530 GAAAAATTTTTCGACGTTTCATCCAAACACCGAAAAAGTAAATCATTTTCAGAAAAAGTA 589
DB 2284 AATTAAATTTTAAATTAATTTAATAATTA-AAAAATAAATTTTATTAATAATTTAA 2226
QY 590 AATCATTTTCAGAAATTAATTTTCGAAATTAATTTTACTGGCAACAATAATGAGTCTAA 649
DB 2225 TTTTATTTTAAATTTTATTTTTCATTTTAAATTTTAAATAAAT---TAAATA 2170
QY 650 GTGTTTCTGTTTAAATTTTAAATTTTTCATTTTAAGAGAAACTAGAAATTGATTTGCAAA 709
DB 2169 TTTTATTTTAAATTTTAAATTTTAAATAAAAAATAAAATTTTAAATAATTTAAATAA 2110
QY 710 TGTCTTTAATCTAGCTTGTAA 731
DB 2109 TAAATTAATAATTAATTAATA 2088
RESULT 5
ABZ10100/c
ID ABZ10100 standard; DNA; 8056 BP.
XX AC ABZ10100;
XX DT 16-JAN-2003 (first entry)
XX DE Haematopoietic cell proliferation disorder related DNA sequence #240.
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX OS Homo sapiens.
XX PN WO200277272-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX WPI; 2003-018942/01.
XX PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX PS Claim 28; SEQ ID NO 240; 117bp; English.
XX CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative

QY 580 CAGAAAAGTAATCATTTTCGAGAAATTAATTTTCGGAATTAATTTACTGCGAAACAAA 639
DB 4528 TATATAAATTAATTTTATGTAATGATAAAATTAATCTACATTATTTTATATATAAATGA 4469
QY 640 TGGAGCTAAGTGTCTGTTTATTTTATTTTCTATTTAGAGAAACTAGAAATTG 699
DB 4468 TGAAGAAAGTTATTTTATTAATAACAAGTAATAATTTTAAATTTTAGATTAGTTAAATG 4409
QY 700 ATTTGTCAATGCTTTAATCTAGCTGTTTGAAGGACAGAAC 754
DB 4408 TTATTTTAAATCTACTTAATTTTCATTAATTAAGATAAAATTAATTTTAAATAATC 4354

RESULT 7

ABV10021/c
ID ABV10021 standard; cDNA; 494 BP.
AC ABV10021;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 10012.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.

XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1; Page 1602; 11750pp; English.

XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX

SEQ Sequence 494 BP; 299 A; 19 C; 21 G; 155 T; 0 U; 0 Other;

Query Match 11.5%; Score 94.2; DB 5; Length 494;
Best Local Similarity 57.2%; Pred. No. 0.0029;
Matches 194; Conservative 0; Mismatches 138; Indels 7; Gaps 1;

QY 134 TTGGTGAATAATGTTAATGGTAGTCTATGTCGAAGTATTTGAGGAGGTGTTAGAA 193
DB 405 TTTTAAATTTTATTAATAATTAATTTTATATATTTTATTAATAATTTTATTA 346
QY 194 TTAATGTTATGGATTACTAATTTCTAGTATTAATGTTGGTGAAGTTAATATAA 253
DB 345 TTTATTTTATTTTATTAATAATTTTATTAATAATTTTATTTTATTTTATTTTA 286
QY 254 TTAATCAATCCTGTTTATTTTATTTTATTAACACAAATTAATAATTTATTAAC 313
DB 285 TAAT-----TTTTTTTATTTTATTTTATTTATTAATTTTATTTTATTTT 233
QY 314 TTTGTTGTTTTCATTTATGAAGTTATATATTTTAGTTAATAATTGACATTAATA 373
DB 232 TTTTATTTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTA 173
QY 374 TATTAATAATAATCAATCTGTAATATATGTAATAATAATTAATAATTAATTAATA 433
DB 172 TATAAATAATAAAATTAATTTATATATTAATAATAATAATAATAATAATAATA 113
QY 434 TATATATTAATAACTCAATCAACAATTAATAATAATAATAATAATAATAATA 472
DB 112 AAAAAATAAAGTAATAATAATAATAATAATAATAATAATAATAATAATAATA 74

RESULT 8

ABL32029
ID ABL32029 standard; DNA; 7351 BP.

AC ABL32029;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 2.

XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antihaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
ds.
XX
KW Homo sapiens.

OS Homo sapiens.
XX
PN WO200200928-A2.

XX
PD 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP007537.

PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

PS Claim 1; SEQ ID NO 2; 32pp + Sequence Listing; German.

XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 7351 BP; 2433 A; 42 C; 1458 G; 3418 T; 0 U; 0 Other;

Query Match 11.1%; Score 90.2; DB 6; Length 7351;
Best Local Similarity 49.4%; Pred. No. 0.0054;
Matches 295; Conservative 0; Mismatches 293; Indels 9; Gaps 2;

QY 140 GAAATGTTAATGCTAGTCTATGTCGAGATTTTCATGGAAGGTGAAGATTAAATG 199
DB 897 GATTATTTTAATAATTTTATGAATTAATAATATTGTAATAAGATATTATTATTA 956
QY 200 TTATTGGGATTAATAATTCTAGTATTATTGTTGGAGGTTAATAATAATTATTC 259
DB 957 TTATTAAAGTATATTAATAAAATTTTAAATGGTTGATATTAAATAATTTT 1016
QY 260 AATCCTGTTTATTTTATTTTATTAACAATAATTAATAATTATTAACTTTGGT 319
DB 1017 TTTTATTTTATTTGAATTTTGAATTTTATGTTAATTATATAGAAATTTTAAAT 1076
QY 320 TGTTCATTTATGACGGTTAATATTAGTTAATAATTGACATTAATATATTA 379
DB 1077 TTTTATTTTAAATAATGTTGATATTATTATTTTATTTGTTAGTATTATAT 1136
QY 380 ATAAATTAATCATTTGTAATATATATGTAATAAATAATTAATAATTAATAATA 439
DB 1137 ATATACGTAT-----GTATATTTATGTTTATATATATATATATGAAATATATATA 1189
QY 440 TAATAAATCAATCAACAATAAATAAGATTAATAATCTTAATATATAATTTTAA 499
DB 1190 TAAATATATATATATGTAATATATATGTTGGTAGGTAATAATTAAATTTTAA 1249
QY 500 ATAGCTTTTCAATAATCTGTCAAACAATAAGAAATTTTTCAGGTTCAATCAACA 559
DB 1250 ATAGAATGTAATTAATAAATTATAAATATTAATAATTTTTCGATTGAGTTAT 1309
QY 560 CCAAGAAAGTAATCATTTTCAGAAAGTAATCATTTTCAGAA--ATATTTTTCGGA 617
DB 1310 AAAATATTTGTATATATATGATTAATAATAAATAAATAAGTATGATTATATAT 1369
QY 618 AATTATTTTACTGCAACAATAAGAGTCTAGTGTCTGTTTATTTTAAATTTTC 677
DB 1370 AGATATAAATAATTAATAATTTTGAAGTATATTTTAAAGAAATGATGAGTTGTT 1429
QY 678 TATTTAGAGAACTAGAAATTTGTCAAATGTCCTTAACTAGCTTTAGAT 734
DB 1430 TTTTAGTGAATTATGATTTATGCAATTTGAAGATTAAATAATTAATTTTGT 1486

RESULT 9
ABL33569
ID ABL33569 standard; DNA; 8305 BP.

XX ABL33569;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1542.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anti anaemic; cyrostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.

XX Homo sapiens.

OS
XX
PN WO200200928-A2.

XX

PD 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP007537.

XX 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

PS Claim 1; SEQ ID NO 1542; 32pp + Sequence listing; German.

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention

XX Sequence 8305 BP; 2163 A; 185 C; 2060 G; 3897 T; 0 U; 0 Other;

Query Match 11.1%; Score 90.2; DB 6; Length 8305;
Best Local Similarity 50.1%; Pred. No. 0.0052;
Matches 284; Conservative 0; Mismatches 273; Indels 10; Gaps 2;

QY 173 TTTCATGGAAGGTGTTAAGAAATTAATGTTATGCGATTACTAATTTCTAGTAAATG 232
DB 1710 TTTTATTTGGGTAATAAGTAAGATTTGTTTATTAATATATATATATATATACGT 1769
QY 233 GGTTCGAAGTTAATAATAATTAATTCATCCCTGTTTATTTTAAACACA 292
DB 1770 ATATACGTATTAT 1829
QY 293 ATTAACAATAATTAATTTAACTTTGTTGTTTCAATTTATGACGGTTAATTTAGTT 352
DB 1830 ATAAATAAATATGTTAATTTATTTTAAAGTAATAAATAATATATATATTTAT 1889
QY 353 TAATAATTGACATTAATATATATTAATAATAAATAAATGTAATATATATATATAT 412
DB 1890 ATATAAATAATATATGTTAATAATAATAATATATATATATATATATTTAAGAAAT 1949
QY 413 TTTAAATATATAATTTATTAATAATAATAAATAAATAAATAAATAAATAAATAA 472
DB 1950 ATTAATTAATATTAATTAATAATAATAATAATAATAATAATAATAATAATAATA 2003
QY 473 AATTCCTAAATATATAAATTTTAAATAAGCTTTTCAGTAAATCTGCAACAATAGAA 532
DB 2004 ATATAATAATAATATATAATAATAATAATAATAATAATAATAATAATAATAATA 2063
QY 533 AATATTTTTCAGGTTCAATCCAAACACGAGAAAGTAATCATTTTCAGAAAGTAAT 592
DB 2064 TATATTAAT---ATATATTATTAATAATAATAATAATAATAATAATAATAATA 2119
QY 593 CATTTTCGAAATTAATTTTCGAAATTAATTTTACTGGCAACAATGAGCTAAGTG 652
DB 2120 TATAATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2179
QY 653 TTTCTGTTTATTTTATTTTCTAATTTAGAGAAACTAGAAATGATTTGCAAAATGT 712
DB 2180 TATATATTTTATTAATATATATATATATATATATATATATATATATATATAT 2239
QY 713 CTTTAATCTAGCTTTAGATTAGTT 739
DB 2240 ATATTATTAGGAGTTGAGATTAGTT 2266

RESULT 10
ABQ67084
ID ABQ67084 standard; DNA; 18357 BP.
XX
AC ABQ67084;
XX
DT 28-AUG-2002 (first entry)
XX
DE Human angiogenesis associated polynucleotide SEQ ID NO 114.
XX
KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
KW inflammation; rheumatoid arthritis; diabetic retinopathy; antitumors;
KW macular degeneration; inflammatory bowel disease; Crohn's disease;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiarteriosclerotic; ds.
XX
OS Homo sapiens.
XX
PN WO200246454-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-EP014320.
XX
PR 06-DEC-2000; 2000DE-01061338.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Schacht O;
XX
DR WPI; 2002-500450/53.
XX
PT New nucleic acid fragments from chemically treated angiogenesis-
PT associated genes, useful for determining methylation status, e.g. in
PT diagnosis or treatment of cancer.
XX
PS Claim 1; SEQ ID NO 114; 41bp + Sequence Listing; German.
XX
CC The invention relates to a nucleic acid (I) comprising a segment of 18
CC bases of chemically pretreated DNA of angiogenesis-associated genes (II)
CC having sequences (ABQ66971-ABQ67178) or their complements. (I), also
CC related oligomers, are used to evaluate the methylation status and/or
CC single-nucleotide polymorphisms, in angiogenesis-related genes, for
CC diagnosis and treatment of eye diseases, proliferative retinopathy,
CC neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
CC diabetic retinopathy, macular degeneration caused by neovascularisation,
CC psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
CC Crohn's disease. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18357 BP; 4920 A; 227 C; 4148 G; 9062 T; 0 U; 0 Other;

Query Match 11.0%; Score 89.8; DB 6; Length 18357;
Best Local Similarity 48.9%; Pred. No. 0.0051;
Matches 302; Conservative 0; Mismatches 307; Indels 8; Gaps 2;

QY 124 GCATTAACGTGTTGGTGAATAATGTTATGCTAGTCTATGCGAAGTATTTTCATGGAAG 183
DB 15286 GTATTATATATTATTAGTGTGTTAGTAGTGTGCGGAGTGTGTTTATAGGAGATGGT 15345
QY 184 GTGTTAAGATTAATGTTATGCGATTACTTAATTTCTAGTATTAATGTTGGAGT 243
DB 15346 TTTATTATTAATAATTAAGATATTAAATTAATTAATTTGTTTATGATTTTAAATGAGGT 15405
QY 244 TAATATATATTAATTAATCAATCCTGTTTATTTTATTTTATTAACACAATTAACAATAA 303
DB 15406 TTATGTTGGAAGTTTATTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTATAT 15465
QY 304 TTTATTAACTTTGTTGTTTCAATTTATGACGGTAAATATTTAGTTTAAATATGAG 363
|||||

DB 15466 TTTTATTGTTGTTATATATGAGTTAGTTATGTTTGGTTTAAATTAGTTGAG 15525
QY 364 CATTATATATATTAATAATAATCAATGTAATATATATGTAATAATAATTAAATATA 423
DB 15526 GTGTTTAAAGAAATTTTAAAGAAATTCGTAATATATATATAATAATTAAGTTA 15585
QY 424 AATTATATATATATATATAATTAACATCAACAATTAATAAAGATATAATCTTAAT 483
DB 15586 GATTATTTTAAATGTTTTTTTATATATGTTGAATTTTCGATTAATTTTTTATAT 15645
QY 484 ATATATAATTTTAAATAGCTTTTCAGTAAATCTGTCAACAAATGAAATATTTTGG 543
DB 15646 AATATAGT-----AATAGATGAAATAATAATATATATATATATGTAATTTTAT 15698
QY 544 CAGTTTCATCCAAACACACAGAAAGTAATCATTTTCAGAAAGTAATCATTTTCAGA 603
DB 15699 TATGTTAATTTTATAGAGAGGATGTAGAGTTTATTTGTATAGTAAATTTTTTAT 15758
QY 604 AATTATTTTCGGAATTAATTTACTGCGCAACAAT-GGAGTCAAGTGTCTGTTT 662
DB 15759 TTTTATGTTTTTTTAAATTTATTTTTTTATTTATTAAGTTTAAAGTTTTTGTGT 15818
QY 663 TATTTTATTTTTCATTTTGAAGAACTAGAAATGATTTGCAATGCTTAAATCTA 722
DB 15819 TATTTTGTGTTTAAATTTTGTGTTTTGTTTTGTTTTGTTTTTATTTATTTT 15878
QY 723 GCTTGTAGATTAGTT 739
DB 15879 TTTTATTTAGTTTTTT 15895

RESULT 11
AAS46429
ID AAS46429 standard; DNA; 6106 BP.
XX
AC AAS46429;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #151.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-BP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
PS Claim 1; SEQ ID NO 151; 27bp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with

CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 U; 0 Other;

Query Match	11.0%;	Score 89.4;	DB 4;	Length 6106;
Best Local Similarity	51.7%;	Pred. No. 0.0069;		
Matches	278;	Conservative	0;	Mismatches 253;
			Indels	7;
			Gaps	3;

OY		198	TGTTATTGGCAATTAACAACTTCTAGTATTAATTGTGGTTTGGAAGTTAATAATAAATTAT	257
Db		2612	TTTTTATTTTAAAGTTTTGTGTTTAAAAGAGTTAAAGAGAAATTATTAAAAATAGTTA	2671
OY		258	TCAATCCTGTGTTTTTATTTTTTTTTTATTAACAACAATTAACAATTAATTAACTTTG	317
Db		2672	TTAATGTTATATTTTAGTCTTTTAAATATATATTAATTAATATATATATTAATAAGTTA	2731
OY		318	GTTGTTTCATTTATGACCGTTAATATTTTGTAGTTTAATTAATGACATTAATATATAT	377
Db		2732	TATATATAATTAATTATATATATAATAATTAATATATGATTAATTTATATATTAATAAAT	2791
OY		378	AAATAAATAAATCATTTGTAATATATGTAAAAATTAATTTAAATATAAATTATTAATTA	437
Db		2792	AATATAATATAATTATATATATATAT-TAATATAATTAATTAATTAATTAATTAATAA	2850
OY		438	TATATAAATACTCAATCAACAACAATAAAGAATAATAAATTCCTAA-----ATATATAAAT	492
Db		2851	TATTAATAATATATTATATATATGATTAATATATAATTATTAATAATTAATTATATAATTA	2910
OY		493	TTTTAAATAAGCTTTTCAGTAATCTGTCACAACAATAGAAAATATTTTTGCAGGTCAT	552
Db		2911	TTATATAATTAATTATATATAATTAATTAATAATTAAATTATATATAATTAATAAATTAAAT	2970
OY		553	CCAAACACCAGAAAAGTAATATCATTTTCAGAAAAGTAATATCATTTTTCAGAAATTATTT	612
Db		2971	-TATATATAATTAATTATAAATTAAATTAATTAATTAATTAATTAATTAATAAGTTTTAT	3029
OY		613	TTCGAATAATTTTACTGCAAAACAATGAGTCTAAGTGTTCTGTTTATTATTTTAT	672
Db		3030	ATATTAATAATTAATATATATTATAATATATAATATAATTAATTAATTTTATTTTATTTT	3089
OY		673	TTTTCTATTTAGAGAACTAGAAATTGATTTGCTCAAATGCTTAACTAGCTGTTT	730
Db		3090	TATAGTATTTTAATATTATTTGTGCTTTAATTGGAAGTATTTGATTAATGATTTGTGTTT	3147

RESULT 12
ABK40031

AC ABK40031;

DT 21-MAY-2002 (first entry)

DE Human chemically pretreated gene sequence #57 strand 1

XX

KM Human; ds, bisulphite treatment; CpG, DNA methylation; cancer; tumour;
KM cytoostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
KM UGT8; MRP; pharmacogenomics; SNP, single nucleotide polymorphism.

OS Homo sapiens.

PN WO200202806-A2

PD 10-JAN-2002.

PF 29-JUN-2001; 2001WO-EP007470.

PR 30-JUN-2000; 2000DE-01032529.

XX

XX

[illegible]

XX
L
L
L
L
L
L
L

PT new nuclear acid, 5-azacytosine methylation state of genes associated with
PT useful for detecting cytosine methylation state of genes associated with
PT pharmacogenomics and for therapy of diseases e.g. cancer.

PS Claim 1; SEQ ID NO 113; 24PP; English.

XX The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1 (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360), MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019862, NM_019898, NM_019899) and their complementary sequences, or a sequence (51) chosen from 87 sequences and their complements. The chemical pretreatment is disulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 U; 0 Other;

Query Match	11.0%;	Score 89.4;	DB 6;	Length 6106;
Best Local Similarity	51.7%;	Pred. No. 0.0069;		
Matches 278;	Conservative	0;	Mismatches 253;	Indels 7;
				Gaps 3;

[illegible]

PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 32; SEQ ID NO 340; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytosolic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligonucleotides are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the pretreated genomic DNA
CC region of the invention. This sequence is not shown within the
CC specification but is taken from Wipoweb.
XX
SQ Sequence 6478 BP; 1878 A; 0 C; 1282 G; 3318 T; 0 U; 0 Other;

Query Match 10.9%; Score 89; DB 9; Length 6478;
Best Local Similarity 51.5%; Pred. No. 0.0076;
Matches 252; Conservative 0; Mismatches 235; Indels 2; Gaps 2;

QY 220 TAGTATTAATTGTTGGAGTTAATATATAATTAATCAATCCTGTTTATTTT 279
DB 4349 TAGTATGGGTTTATTAATAATGATAATATTTGTTAGTTAATTAATTTTATATG 4408
QY 280 TTTTATTAACACAAATTACAAATTAATTTTAACTTGGTGTTCATTTATGACGGT 339
DB 4409 AATTAAATGTTGATAGTAAATTAAGAGTTA-TTATTTAAATTTAAGTATTAATTTATA 4467
QY 340 TAAATTTTGTAGTTAATTAATGACATTAATATATATTAATTAATTAATCAATGTAATA 399
DB 4468 AATTAAGATTATGATTAGTATATGTTAATTAATTTTATTAATTAATTAATTTATTTT 4527
QY 400 TAATGTAATAAATTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 459
DB 4528 TTTGAAAATTTGATTGTTTATTAATTTTATTTTAAAGTAAATAAGAAAGAAATATA 4587
QY 460 TAAAAAGATAATTAATCTTAATAATTAATTAATTTTAAATAGCTTTTCAGTAATCTG 519
DB 4588 TAAATTAAGTTAATTTTAAATTAATTAATTTGTTGTTATTAATTAATTAATTAATTA 4647
QY 520 TCAACAATAGAAAATATTTTTCGAGGTTCAATCCAAACACGAGAAAAGTAATCATTTT 579
DB 4648 AGAAAGTGAAAATAGATTGATTGTTGTAATGAATGAATTAATTAATTAATTTT 4707
QY 580 -CAGAAAGTAATCAATTTTTCAGAAATTAATTTTCGAAATTAATTTTCTGCAACAA 638
DB 4708 AATATATGTTAATAGGTTGGAAGAAATTTTAAATATTTTGTGTAATGATATAAA 4767
QY 639 ATGAGTCTAAGTCTTCTGTTTATTTTATTTTCTATTTAGAGAACTAGAAAT 698
DB 4768 TAATATTTGATATGTTGTTATTTTATTTTGTGTTGATTAATGAATTAATAAATG 4827
QY 699 GATTGTCA 707
DB 4828 TATTTTAA 4836

RESULT 15
ABL32727
ID ABL32727 standard; DNA; 16602 BP.
XX
AC ABL32727;
XX
DT 26-MAR-2002 (first entry)

XX
DE Human immune system associated gene SEQ ID NO: 700.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosolic; noctropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
ds.
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

Claim 1; SEQ ID NO 700; 32pp + Sequence listing; German.
The present invention provides a number of human immune system associated
genes which are modified by the methylation of cytosines. The sequences
can be used in the diagnosis and treatment of immune system disorders,
including eye diseases such as retinopathy, neovascular glaucoma and
macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
diseases. The present sequence is a gene of the invention

Query Match 10.8%; Score 88.2; DB 6; Length 16602;
Best Local Similarity 48.8%; Pred. No. 0.008;
Matches 301; Conservative 0; Mismatches 308; Indels 8; Gaps 2;

QY 124 GCATTAACCTGTTGGTGAATAATGTTAATGTTAGTCTAATGCAAGTATTTTCATGGAAG 183
DB 15284 GTATTAATTAATTTATGTTGTTGTTAGTAGTGTGCGGAGTTGTTTATAGAGATGCT 15343
QY 184 GTGTTAAGAAATTAATGTTATTTGGCATTAATTTCTAGTAATTAATTTGTTGGAAGT 243
DB 15344 TTTATTAATTAATTAAGATATTAATTAATTAATTTGTTTATGAATTTTAAATGAGGCT 15403
QY 244 TAATATTAATTAATTTCAATCCTGTTTATTTTATTTTATTAACACAAATTAACAAATA 303
DB 15404 TCGTGTGGAAGTTTATTTGTTTATTTTGTGTTTGGTAATTTAATGTTTGTGTAAT 15463
QY 304 TTTATTTAATTTGTTGTTTCAATTTATGACGGTTAATATTTTATTAATTAATTTGAG 363
DB 15464 TTTTATTTATTTGTTATATATAGGTTAGTTATTTGTTGTTTAAATTAATGTTGAG 15523
QY 364 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 423
DB 15524 GTGTTTAAAGAAATTTTAAAGAAATTTGTAATAATTAATTAATTAATTAATTAAT 15583
QY 424 AATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 483
DB 15584 GATTATTTAAATGTTTATTTTATTTATATGATGAATTTGATTAATTTTATATAT 15643

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 20:44:50 ; Search time 81 Seconds
(without alignments)
5590.616 Million cell updates/sec

Title: US-10-089-557-2_COPY_1_816

Perfect score: 816
Sequence: 1 actataggcgacgcgtgtc.....tatttcagtattgtaaaag 816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.2	10.8	5852	1	US-07-867-106-2
2	82.4	10.1	665	2	US-08-883-795A-36
3	78.4	9.6	6124	4	US-08-213-419B-3
4	78	9.6	5852	1	US-07-867-106-2
5	77	9.4	5152	4	US-10-204-708-74
6	76.2	9.3	665	2	US-08-883-795A-36
7	75.8	9.3	5455	4	US-10-204-708-33
8	75.6	9.3	6156	4	US-10-204-708-60
9	75.2	9.2	20674	4	US-09-641-638-651
10	74.8	9.2	5152	4	US-10-204-708-73
11	74.4	9.1	6669	4	US-10-204-708-6
12	74.2	9.1	2058	2	US-08-749-391-1
13	74.2	9.1	2058	3	US-09-390-200-1
14	73.8	9.0	20674	4	US-09-641-638-651
15	73.6	9.0	6070	4	US-10-204-708-10
16	73.2	9.0	19124	2	US-08-487-826B-13
17	73.2	9.0	640681	4	US-09-790-988-1
18	73	8.9	11049	4	US-10-204-708-22
19	72.2	8.8	3701	3	US-08-845-258-10
20	72.2	8.8	3701	3	US-08-990-571-10
21	72.2	8.8	3701	4	US-08-723-142A-10
22	72.2	8.8	3701	4	US-09-528-784A-10
23	72.2	8.8	3701	4	US-09-569-098A-10
24	72.2	8.8	6243	2	US-09-056-075-1
25	72	8.8	53332	4	US-09-801-861-3
26	71.8	8.8	834	3	US-08-998-416-305
27	71.8	8.8	5152	4	US-10-204-708-73

28	71.6	8.8	7832	4	US-09-004-838-94	Sequence 94, Appl
29	71.2	8.7	6317	4	US-10-204-708-11	Sequence 11, Appl
30	71.2	8.7	26000	4	US-09-843-376-10	Sequence 10, Appl
31	70.8	8.7	10640	4	US-09-417-485D-5	Sequence 5, Appli
32	70.6	8.7	5152	4	US-10-204-708-74	Sequence 74, Appl
33	70.6	8.7	6317	4	US-10-204-708-11	Sequence 11, Appl
34	70.4	8.6	2435	3	US-09-306-593-1	Sequence 1, Appli
35	70.4	8.6	10467	4	US-10-204-708-2	Sequence 2, Appli
36	70.4	8.6	640681	4	US-09-790-988-1	Sequence 1, Appli
37	70.2	8.6	1441	4	US-08-956-171E-1000	Sequence 1000, Ap
38	69.6	8.5	615	3	US-08-998-416-186	Sequence 186, App
39	69.6	8.5	837	3	US-08-998-416-288	Sequence 288, App
40	69.6	8.5	1511	1	US-07-991-867B-8	Sequence 8, Appli
41	69.6	8.5	1511	1	US-08-107-755A-8	Sequence 8, Appli
42	69.6	8.5	1511	2	US-08-544-332-8	Sequence 8, Appli
43	69.6	8.5	1511	4	US-09-370-861A-8	Sequence 8, Appli
44	69.4	8.5	11049	4	US-10-204-708-23	Sequence 23, Appl
45	69	8.5	642	1	US-08-764-100-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-07-867-106-2
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
; FEATURE:
; NAME/KEY: CDS

Db 5490 CAATAACATATTTGATTTTTTTTTTTTTTTTTTTTTTTTAAATAATCAATAATTT 5431
QY 626 TACTGGCAACAAATGGAGTCTAAGTGTTCGTTTTTAT--TTTTATTTTCTATTTA 683
Db 5430 AAATAATTTATCTATATATCTTGATGACCTTCAATTTTATTAATTTAATATTAAATTT 5371
QY 684 GAGAACTAGAAATTTGATTGTCGAATGCTTTTAACTAGCTTGTTAGATTAGTTGAAG 743
Db 5370 TAAAAATTTAGTCTATCGATCTATATAATTTTCCATGTTTAAATTTTAAAG 5311

RESULT 5

US-10-204-708-74/c
; Sequence 74, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 74
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-74

Query Match 9.4%; Score 77; DB 4; Length 5152;
Best Local Similarity 49.7%; Pred. No. 1.8e-05;
Matches 252; Conservative 0; Mismatches 250; Indels 5; Gaps 2;

QY 225 TTAATGTGTTTGAAGTTAATATATAATTAATCAATCCTGTTTATTTTATTTT 284
Db 2165 TTAATAACCAATTCACACAAATCACTTTAATACTAACAACAACACTTTTACCATATAA 2106
QY 285 ATAACAATTAACAATAATTAATTTAACTTTGGTGTTCATTATTAAGCGGTTAATA 344
Db 2105 ATTTTATATATATATATATTTAATACTTATTACTTTATATATTAATTAATTAATT 2046
QY 345 TTTTGTATTAATTAATGAGCATTAATTAATTAATAATAATAATCAATGTAATATATGT 404
Db 2045 TTTTAAATACCTACTATTAATTTAACAATTAATACTAAACACATAAATAAATAAATAA 1986
QY 405 AAAAATAAT--TAAATATTAATTTATTAATATATATAATAAATCAATCAACAATA 461
Db 1985 CATATCTCTCTCTAAATAAATTTCAATATCTTATCAACAACAACAACAATAAATAA 1926
QY 462 AAAAGATTAATTAATTTAATATATAATAATTTTAAATAAGCTTTTCAGTAATCTGTC 521
Db 1925 ATAAAAACACTAAACTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1866
QY 522 AAACAATAGAAAAATTTTTCAGGTTCATCCAAACACAGAAAAAGTAATCAATTTTCA 581
Db 1865 AATATATCTTAATAATTTTTCACAAATAATTTTAAATAATCACTAATAACTTAATTTTAA 1806
QY 582 GAAAAAGTAA--ATCATTTTTCAGAAATTAATTTTTCGAAATTAATTTTACTGCAAAACAA 639

Db 1805 AATAAACCACTATTAAACATTTTAAATAATTTTATTACAAATTACTTCCAAAATTACCTC 1746
QY 640 TGGAGCTTAAGTGTTCGTTTATTTTATTTTCTATTATTAGAGAACTAGAAATTTG 699
Db 1745 GTTAATGCAAAATACTTATCTTACGATCCATTTTAAATATCTAATAAATAAATAAATAA 1686
QY 700 ATTGTCAATGCTCTTAACTAGCTT 726
Db 1685 AAAAAACAATAAATTAATAATAATTT 1659

RESULT 6

US-08-883-795A-36
; Sequence 36, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: Rh 32
US-08-883-795A-36

Query Match 9.3%; Score 76.2; DB 2; Length 665;
Best Local Similarity 47.1%; Pred. No. 2.1e-05;
Matches 268; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 184 GTGTTAAGAATTAATGTTATTTGGGATTAATTTCTAGTATTAATTGTGTTGGAAGT 243
Db 20 GTTTTATATAATTAATAATTTTATTAATTTAAATAATTTAATAATTAATAATTAATA 79
QY 244 TAATATATAATTAATCAATCCTGTTTATTTTATTTTATTAACACAATTAACAATAA 303
Db 80 TATTTTATTAATTAATAATTTTATTAATTAATAATAATTTTATTAATAATAATAA 139
QY 304 TTTATTTAATCTTTGTTGTTTCAATTTAAGCGTTAATATTTTATTAATAATTTAG 363
Db 140 TATTTTATTAATTAATAATTTTATTAATTAATAATTTTATTAATAATAATAATTTAATTT-- 196


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OY 364 CATATATATATTAATAATAAATCATGTAATATATGTAAAAATTAATTTAAATATA 423
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Db 197 AAATATTTTATTAATAAATATTTATTAATAAATATTTTATTAATAAATATTTAAT 256
OY 424 AATTATTAATATATTAATAAATCAATCAACAATAAAGATAAATAATCTTAAT 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 AAATATTTTATTAATAAATGTTTATTAATTAATAATTTTATTAATAAATGTTTAAAT 316
OY 484 ATATAAATTTTAAATAGCTTTTCAGTAATCTGTCAACAACATAGAAAATATTTTGG 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 ACATATTTTATTAATAAATGTTTATTAATTAACATATTTTATTAATAAATGTTTAAAT 376
OY 544 CAGGTCATCCAAACACGAAAGTAATCAATTTTCAGAAAAGTAATCAATTTTCAGA 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 ACATATTTTATTAATAAATGTTTATTAATTAACATATTTTATTAATAAATGTTTAAAT 436
OY 604 AATTATTTTTCGGAATTAATTTTACTGCAACAACAAATGAGTCTAGTGTTCGTTTTT 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 ACATATTTTATTAATTAACATATTTTATTAAGTATTTATTAATTAACATATTTTAAATTAAG 496
OY 664 ATTTTTATTTTCTATTTAGAGAACTAGAATTTGATTTGCAATGCTTTAATCTAG 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 TATTATTAATTAACATATTTTATTAAGTATTTTATTAATTAACATATTTTAAATCTAAT 556
OY 724 CTGTTAGATTAGTTGAAGGGCAGAGAA 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 ATTTTAAATAGTTAAAAAGACGAGGAA 585
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RESULT 7

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US-10-204-708-33
; Sequence 33, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 33
; LENGTH: 5455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-33
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Query Match 9.3%; Score 75.8; DB 4; Length 5455;
Best Local Similarity 46.7%; Pred. No. 2.9e-05;
Matches 274; Conservative 0; Mismatches 312; Indels 1; Gaps 1;
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OY 160 TATGTCGAAGTATTTTCATGGAAGGTGTTAAGAAATTAATGTTATTTGGGATTAATAATTC 219
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Db 568 TTTTATTAATTTTGTGGTAGTACGTTAAATTTACGTTTTTGTATTTTATTTT 627
OY 220 TAGTATTAATTTGTTGGAAGTTAATATATTAATTAATCAATCCTGTTTATTTT 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 628 TTGTTTTTTTTTTAGTTTGGGATATTTAATGTTATTCGATTTATTTTATTTAGTTTGT 687
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OY 280 TTTTATTAACACAATTTACAAATTAATTTTAACTTTGGTGTTCATTTATGACGGT 339
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Db 688 TTTTAAATTTTCGATTTTAGTTTTGTGTTTGTTCGTTTTTTTAAAGTTTAAATTTA 747
OY 340 TAATATTTTA-GTTTAATTAATTGAGCATTAATTAATATTAATTAATAAATCAATGTAAT 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 TTGTTTTTATTTTAAAGTTTAAATATATATCGTTTTTTTGAAGCGTTTTTATTTAT 807
OY 399 ATATGTAATAAATTTTAAATATATAATTTTAAATATATATATTAATTAACATCAACA 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 808 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 867
OY 459 ATAAAAAGATAATAATTTCTTAATATATAAATTTTAAATAGCTTTTCAGTAATCT 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 868 TTTTAGATTTTGTAGGATATATGTTTAAATGAGGTTTTTTTTTGTGTTTTTAAAT 927
OY 519 GTCAACAATAGAAAATATTTTTCAGAGTTCAATCCAAACACGAAAGTAATCAATTT 578
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 928 TTGTTGGGTTTATGTTTATTTTATTTATTTAGTTCGTTTTTAAATTTTATTTAGTTTAAAT 987
OY 579 TCAGAAAAGTAATCAATTTTTCAGAAATTAATTTTCGAAATTAATTTACTGCAACAA 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 988 TTGGGAATTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1047
OY 639 ATGAGCTCTAAGTGTTCGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 698
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 ATAAATTTTATAGGTTGATTTTGAATTTTATTTATTTGTTAATAAGTTAATGTTT 1107
OY 699 GATTGTCAATGCTCTTAATCTAGCTGTTAGATTAGTTGAGG 745
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Db 1108 TTTTAAATTAATTTTATTTAATAAGAGTGTACGTGGATTGGGG 1154
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RESULT 8

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US-10-204-708-60
; Sequence 60, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 60
; LENGTH: 6156
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-60
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Query Match 9.3%; Score 75.6; DB 4; Length 6156;
Best Local Similarity 49.0%; Pred. No. 3.2e-05;
Matches 291; Conservative 0; Mismatches 294; Indels 9; Gaps 3;
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OY 155 AGTGTATGTGCAAGTATTTTCATGGAAGGTGTTAAGAAATTAATGTTATTTGGGATTAATA 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 522 ATTGTATTTGTTTATTAATAGTTTATTAATAATTAATTAATTTGTTAGATTTTGTA 5281
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QY 215 ATTTCTAGTATTAATGTGGTTTGAAGTTAATATAATTAATTCATCCCTGTTT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5282 AATTGGAGTGTGAATAT--TTAGTATTTGTTGTTTATCGTTATTTGTTAGTGT 5339
QY 275 TTTTCTTTTAAACACAATTACAATAATTAATTTAACTTTGTTGTTTCAATTTATG 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5340 ATATATTTTAAAGTTTCTTTTAAATAATTTATATTTATTTAGGTTTAAAGATT 5399
QY 335 ACGTTAATTTTGTAGTTAATATGAGCATTTATATATTAATAATAATCAATG 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5400 TTTTCTTTTGGTTGATTAGATTGGGATGTTGTTTATTTATATATATATATA 5459
QY 395 TA-ATAATGTAAATAATTAATAATAATTTATTAATATATAATAACTCAATC 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5460 TAGATATATGATATATATATGATATATATATGTTGATATATATATATATATATG 5519
QY 454 AAACAATAAAAGATAA-----TAAATCTTAATATATAAATTTTAAATAGCTTT 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5520 TTACATTTAAAGATAAATATTTTAAATTTATTTGATATATAAATAATTAATTTAGTTT 5579
QY 508 TCAGTAAATCTGTCAACAATAGAAAATATTTTTCAGAGTTCAATCCAAACACGAAAA 567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5580 TTATTAATTATTAAAGTAAGATTAGTTAGTAGATTGTTTATTTGTAATGATA 5639
QY 568 GTAAATCATTTTCAGAAAGTAAATCATTTTCAGAAATTAATTTTCGGAATTAATTTTA 627
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Db 5640 TTTTAAAGTTTATTTATTTTAAAGTTGATGATTAATAAGATGATATATATATGTAATT 5699
QY 628 CTGGCAACAAGAGCTAAGTCTTCTGTTTATTTTATTTTATTTTCAATTTAGAGA 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5700 GAGTATATTTTAAATTAATTAAGTTTCTGTTGTTTATTTTATTTTATTTTATAGT 5759
QY 688 AACTAGAATGATTTGTCAATGCTTTAATCTAGCTGTTTAGATTAGTTGA 741
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Db 5760 TAATTATTTAAATAAGATGATGTTATGATTTTGTATATTTAATAATTTTAA 5813
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RESULT 9
US-09-641-638-651/c
: Sequence 651, Application US/09641638
: Patent No. 6432648
: GENERAL INFORMATION:
: APPLICANT: Blumenfeld, Marta
: APPLICANT: Bougueleret, Lydie
: APPLICANT: Chumakov, Ilya
: APPLICANT: Cohen, Annick
: TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
: FILE REFERENCE: GENSET.051CPI
: CURRENT APPLICATION NUMBER: US/09/641,638
: PRIOR FILING DATE: 2000-08-16
: PRIOR APPLICATION NUMBER: US 09/502,330
: PRIOR FILING DATE: 2000-02-11
: PRIOR APPLICATION NUMBER: US 60/133,200
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: US 09/275,267
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: US 60/119,917
: PRIOR FILING DATE: 1999-02-12
: NUMBER OF SEQ ID NOS: 1304
: SOFTWARE: Patent.pm
: SEQ ID NO 651
: LENGTH: 20674
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1123..3123
: OTHER INFORMATION: 5'regulatory region
: NAME/KEY: exon
: LOCATION: 3124..3297
: OTHER INFORMATION: exon 1
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: NAME/KEY: exon
: LOCATION: 3871..4072
: OTHER INFORMATION: exon 2
: NAME/KEY: exon
: LOCATION: 5552..5633
: OTHER INFORMATION: exon 3
: NAME/KEY: exon
: LOCATION: 5758..5880
: OTHER INFORMATION: exon 4
: NAME/KEY: exon
: LOCATION: 5996..6099
: OTHER INFORMATION: exon 5
: NAME/KEY: exon
: LOCATION: 6349..6509
: OTHER INFORMATION: exon 6
: NAME/KEY: exon
: LOCATION: 7379..7522
: OTHER INFORMATION: exon 7
: NAME/KEY: exon
: LOCATION: 8645..8854
: OTHER INFORMATION: exon 8
: NAME/KEY: exon
: LOCATION: 12254..12340
: OTHER INFORMATION: exon 9
: NAME/KEY: exon
: LOCATION: 12854..13023
: OTHER INFORMATION: exon 10
: NAME/KEY: exon
: LOCATION: 13308..13429
: OTHER INFORMATION: exon 11
: NAME/KEY: exon
: LOCATION: 16567..16667
: OTHER INFORMATION: exon 12
: NAME/KEY: exon
: LOCATION: 16775..16945
: OTHER INFORMATION: exon 13
: NAME/KEY: exon
: LOCATION: 17063..17554
: OTHER INFORMATION: exon 14
: NAME/KEY: misc feature
: LOCATION: 17555..20674
: OTHER INFORMATION: 3'regulatory region
: NAME/KEY: allele
: LOCATION: 1128
: OTHER INFORMATION: 10-508-191 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1182
: OTHER INFORMATION: 10-508-245 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1559
: OTHER INFORMATION: 10-509-284 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 1570
: OTHER INFORMATION: 10-509-295 : deletion of C
: NAME/KEY: allele
: LOCATION: 1827
: OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
: NAME/KEY: allele
: LOCATION: 2048
: OTHER INFORMATION: 10-511-62 : polymorphic base C or T
: NAME/KEY: allele
: LOCATION: 2323
: OTHER INFORMATION: 10-511-337 : insertion of T
: NAME/KEY: allele
: LOCATION: 2341
: OTHER INFORMATION: 10-512-36 : polymorphic base G or C
: NAME/KEY: allele
: LOCATION: 2623
: OTHER INFORMATION: 10-512-318 : polymorphic base A or G
: NAME/KEY: allele
: LOCATION: 2832
: OTHER INFORMATION: 10-513-250 : polymorphic base A or G
: NAME/KEY: allele
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/	LOCATION:	2844		:	polymorphic base C or T
/	OTHER INFORMATION:	10-513-262		:	
/	NAME/KEY:	allele		:	
/	LOCATION:	2934		:	
/	OTHER INFORMATION:	10-513-352		:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	2947		:	
/	OTHER INFORMATION:	10-513-365		:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	3802		:	
/	OTHER INFORMATION:	12-206-81	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	4062		:	
/	OTHER INFORMATION:	10-343-231	:	:	deletion of C
/	NAME/KEY:	allele		:	
/	LOCATION:	4088		:	
/	OTHER INFORMATION:	12-206-366	:	:	polymorphic base C or T
/	NAME/KEY:	allele		:	
/	LOCATION:	4109		:	
/	OTHER INFORMATION:	10-343-278	:	:	polymorphic base C or T
/	NAME/KEY:	allele		:	
/	LOCATION:	4170		:	
/	OTHER INFORMATION:	10-343-339	:	:	polymorphic base G or T
/	NAME/KEY:	allele		:	
/	LOCATION:	5903		:	
/	OTHER INFORMATION:	10-346-23	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	6019		:	
/	OTHER INFORMATION:	10-346-141	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	6141		:	
/	OTHER INFORMATION:	10-346-263	:	:	polymorphic base G or C
/	NAME/KEY:	allele		:	
/	LOCATION:	6183		:	
/	OTHER INFORMATION:	10-346-305	:	:	polymorphic base C or T
/	NAME/KEY:	allele		:	
/	LOCATION:	6338		:	
/	OTHER INFORMATION:	10-347-74	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	6375		:	
/	OTHER INFORMATION:	10-347-111	:	:	polymorphic base G or C
/	NAME/KEY:	allele		:	
/	LOCATION:	6429		:	
/	OTHER INFORMATION:	10-347-165	:	:	polymorphic base C or T
/	NAME/KEY:	allele		:	
/	LOCATION:	6467		:	
/	OTHER INFORMATION:	10-347-203	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	6484		:	
/	OTHER INFORMATION:	10-347-220	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	6534		:	
/	OTHER INFORMATION:	10-347-271	:	:	polymorphic base A or T
/	NAME/KEY:	allele		:	
/	LOCATION:	6611		:	
/	OTHER INFORMATION:	10-347-348	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	7668		:	
/	OTHER INFORMATION:	10-348-391	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	8608		:	
/	OTHER INFORMATION:	10-349-47	:	:	polymorphic base C or T
/	NAME/KEY:	allele		:	
/	LOCATION:	8658		:	
/	OTHER INFORMATION:	10-349-97	:	:	polymorphic base A or G
/	NAME/KEY:	allele		:	
/	LOCATION:	8703		:	
/	OTHER INFORMATION:	10-349-142	:	:	polymorphic base G or C
/	NAME/KEY:	allele		:	
/	LOCATION:	8777		:	
/	OTHER INFORMATION:	10-349-216	:	:	deletion of CTG
/	NAME/KEY:	allele		:	
/	LOCATION:	8785		:	

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? OTHER INFORMATION: 10-349-224 : polymorphic base G or T
? NAME/KEY: allele
? LOCATION: 8926
? OTHER INFORMATION: 10-349-368 : polymorphic base C or T
? NAME/KEY: allele
? LOCATION: 12171
? OTHER INFORMATION: 10-350-72 : polymorphic base C or T
? NAME/KEY: allele
? LOCATION: 12429
? OTHER INFORMATION: 10-350-332 : polymorphic base C or T
? NAME/KEY: allele
? LOCATION: 13341
? OTHER INFORMATION: 10-507-170 : polymorphic base A or G
? NAME/KEY: allele
? LOCATION: 13492
? OTHER INFORMATION: 10-507-321 : polymorphic base A or C
? NAME/KEY: allele
? LOCATION: 13524
? OTHER INFORMATION: 10-507-353 : polymorphic base C or T
? NAME/KEY: allele
? LOCATION: 13535

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Query Match	9.2%;	Score 75.2;	DB 4;	Length 20674;
Best Local Similarity	50.4%;	Pred. No. 4.2e-05;		
Matches 266;	Conservative	0;	Mismatches 253;	Indels 9;
				Gaps 3;

OY	162 TGTGGAAGTATTTTCATGGAAAGTGTTAAGAATTAAATGTAATTGGGATTAATACTAATTTCTA	221
Db	11581 TAATGAAAAAAGGCCATGGCTTTTTTTTAATATTAATAATTTCCCTTAGCTATTAATAAT	11522
OY	222 GTATTAATTTGTGTTTGGAAGTTAATATATATTAATTAATCAATCCTGTTTTTTTAATTTTTT	281
Db	11521 TTAAATATTAATAATTTAAATTAATTAATATTAATAATATTTAAATTTAAATTTAAAT	11462
OY	282 TTTATACACAATTTACAAATAATTTAATTTAACTTTGGTTGTTTCAATTTATGACGGTTA	341
Db	11461 TTAATATTAATAATTAATAATATTAATAATTTAATTTAATATGGAACAATTAA-----AATT	11407
OY	342 ATATTTTAGTTTAATTAATTTGAGCATTAATATATATTAATTAATAATTAATCATTTGTAATATA	401
Db	11406 AAAATTAATAATTAATTAATATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAATA	11347
OY	402 TGTAATAATAATTTAAATAATATAATTTAATTAATATATTAATTAATACTCAATCAACAATA	461
Db	11346 TTAATAATTTAAATTTAATAT-TAAATTAATTAATAATTAAGTTAAATTAATATTAATAATTAAT	11288
OY	462 AAAAGATATAATAATCTTBAATATATTAATAATTTTTTAAANAAGCTTTTCAGTAAATCTGC	521
Db	11287 TAAGTTAAATTTAATATTTAAATTTAAATTTAATTTAATAATTTAAAAATTTAAATGTTT	11228
OY	522 AAACAATAGAAAATATTTTTTTCAGAGTTTCATCCAACACCAGAAAAAGTAAATCATTTTCA	581
Db	11227 ATTTAAAAATTAATTTAATAATTTTAAAAATTTA--AATTTATTTAAATTTTAAATTAATTTAAT	11171
OY	582 GAAAAATTAATCATTTTTCAGAAATTAATTTTTCGGAAATTAATTTTACTGGCAACAACAATG	641
Db	11170 TAAAAATTAATAATTTTAATTTAAATTAATAATTTAAAAATTTTAATTTTAATTAATTAATAATTTAAAA	11111
OY	642 GAGTCTAGTGTCTGTTTTTATTTTAAATTTTCTATTTAGAGAA 689	
Db	11110 TTTATTAATAATTAATAATATTTTAAATATTTTCCCTTAGCTATTAAAAAA 11063	

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RESULT 10
US-10-204-708-73
; Sequence 73, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation

```



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; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-73
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Query Match          9.2%; Score 74.8; DB 4; Length 5152;
Best Local Similarity 49.6%; Pred. No. 4.4e-05;
Matches 277; Conservative 0; Mismatches 272; Indels 9; Gaps 3;
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QY 173 TTTCATGGAAGGTGTTAAGAAATTAATGTTATGGGATTAATAATTCTAGATTAATTTGT 232
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Db 2942 TTTTAATAATTAATTTGAAAAATGTAATTATTAGTTGTAATATTTPAATAGTTAGTTT 3001

QY 233 GGTTCGGAAGTTAATATAATTAATTAATCAATCCCTGTTTATT--TTTTTTATAACA 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3002 TATATAAATTAATTTTAATTAATTTGTAATAATTTTATATGTTGGTTTATATATATA 3061

QY 291 CAATTACAATAATTAATTAATTAATCTTGGTTGTTTCAATTTATGACGTTAATAATTTAG 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3062 TATGTTAATGATTTAATTTAATTTATATATATGTTGATTAATTTTGGAGTTTAT 3121

QY 351 TTTAATAATGAGCATTTATATATTAATAATAAATCATTTGTAATATATATAATAAAT 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3122 TATGATTTAGTATAATTAATTAATTAATGAGGTTAAAAATGGG----ATAATAATTTT 3176

QY 411 AATTTAAATATAATTTAATTAATATATATATAAATCAATCAACAATAATAAAGATAA 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3177 TTTTGGAGGAATTTAATAATGTTTGTAGTAATAAATAAGAAATGATGAGTAT 3236

QY 471 TAAATCTTAATAATATAATTTTAAATAAGCTTTTCAATAATCTGCAACAATAG 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3237 TAAATGTGAGAGATAAATAATTTGGAAGATTAGTTAATGAAGTTAATAAATGCTTT 3296

QY 531 AAAATATTTTTCAGAGTTCATCCAAACACCAAGAAAGTAAATCATTTTCAGAAAAGTAA 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3297 GAATAGTTTAAATAATAATTTTAAAGTTATGAAATGATTAGTTTGAATAAGTTA 3356

QY 591 --ATCATTTTTCAGAAATTAATTTTCGAAATTAATTAATGCAACAACAATGAGTCTA 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3357 TTGTTAATATTTTAAATAATTTTGTGTAATTAATTTTAAATTAATTCGTTAATTA 3416

QY 649 AGTGTTCGTTTATTTTATTTTCTATTTAGAGAACTAGAAATGCAATTTGTCAA 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3417 AAATAGTTTATTTTACGATTTATTTAGTATTTAGAAAAAGAAAAAGAAAAAGTAA 3476

QY 709 ATGCTTTAATCTAGCTT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3477 GTAATTAAGGTGATTT 3494
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RESULT 11
US-10-204-708-6
; Sequence 6, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
```

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; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 6
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-6
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Query Match          9.1%; Score 74.4; DB 4; Length 6669;
Best Local Similarity 48.4%; Pred. No. 5.2e-05;
Matches 237; Conservative 0; Mismatches 251; Indels 2; Gaps 1;
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QY 184 GTGTTAAGAATTAATGTTATTTGGATTACTAATTTCTAGTATTAATTTGGTTGGAAGT 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6057 GTATTTATTGTAATTTTAAATATATATATAATTTTAAAGTTAGTAGTGTTTTTAGT 6116

QY 244 TAATATATAATTAATCAATCCTGTTTATTTTATTTTATTAACACAAATTAATAATA 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6117 TTTTATTTTATTAAGAGTAGTATTGTTTATTTTATTTTATTTTGTGTTGTAATTA 6176

QY 304 TTTATTTAATTTGTTGTTTCAATTTATG--ACGGTTAATTTTATTTTATTAATTTG 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6177 GTTAATTTGTAATAATTTTATTTTATTTTAAAGTAATAATTTTATTAAGTAAGAAATTT 6236

QY 362 AGCATTAATTAATTAATAATAATAATCAATGTAATATATGTAATAATAATAATAATA 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6237 GTTTTGTATTTGTAATTTAGTAATATAAGATAATAATAAGTACGTTTAAAGAAAT 6296

QY 422 TAAATTTAATTAATATAATAATAATACTCAATCAACAATAAAGATAATAATCTTAA 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6297 TATTTGATGTTTAAAGAAATTAATAATTAATTTTAAAGAAATAATAATATGAGT 6356

QY 482 ATATATAAATTTTAAATAAGCTTTTCAGTAATCTGTCACAACAATAGAAATAATTTT 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6357 AAGGAGATGTTTATATAAGCGTGTATTATTAATTTTGTGTTTAAATTTTATTTT 6416

QY 542 TGCAGTTCATCCAAACACCAAGAAAGTAATCAATTTTCAGAAAGTAATCAATTTTCA 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6417 TATTTTATTTTATTAAGTAGAAGAAATAATTTTATATATAGTTAGCAATTTTAT 6476

QY 602 GAAATTAATTTTCGAAATTAATTTTACTGCGCAACAATGAGTCTAAGTCTTCTGTT 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6477 TTTTATTTTATTTTTCGCTGTTTATTTTATTAATTTTATTTAGTATTTATTAATTTT 6536

QY 662 TTATTTTAA 671
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Db 6537 ATTTATAATA 6546
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RESULT 12
US-08-749-391-1
; Sequence 1, Application US/08749391
; Patent No. 5948667
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
```

```

; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2058 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neocallimastix patriciarum
; STRAIN: 27
; IMMEDIATE SOURCE:
; LIBRARY: genomic DNA library
; CLONE: pNspX-06
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 301..1755
; US-08-749-391-1

Query Match          9.1%; Score 74.2; DB 2; Length 2058;
Best Local Similarity 54.7%; Pred. No. 5.1e-05;
Matches 168; Conservative 0; Mismatches 138; Indels 1; Gaps 1;

QY 185 TGTTAAGATTAATGTTAATGGGATTAATTTCTAGTATTAATTGTTGGAAAGTT 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1747 TGTCAAAAATAAATGATTAAGAAATCATTAATCAACCATATTTATTTGATTAATAAAT 1806

QY 245 AATATATATTAATTAATCAATCCTGTTTTTATTTTTTTTATTAACACAAATTAATAAT 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1807 AATAAAGAAAAAATAAATTTTTTTTATTTTTTTTCTCCCAATTAATAAA 1866

QY 305 TTATTTACTTTGGTGTTCATTTTGAACGGTTAATTTTGAAGTTAATTAATGAGC 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1867 TCATTAATAATAGATCATTAATATAATTAATTTTCAATTTTTTTTTTTTAATAATA 1926

QY 365 ATTATTAATTAATAATAAATCAATGTAATATATGTAATAAATAATTTAAATAATA 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1927 CGTAATGTAATGTAATTTAAACAATTTAATATTTAATATTTTATAAAGAT-A 1985

QY 425 ATTTATTAATATATATAAATACTCAATCAACAATAAAGATAATAATCTTAATA 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 1986 CTATTTTAATAAAATTATAAAAAAATATATAAAAAAATATAAAAAAATATAAAAAA 2045
QY 485 TATAAAT 491
    ||| |||
Db 2046 TATTAAT 2052

RESULT 13
US-09-390-200-1
; Sequence 1, Application US/09390200
; Patent No. 6137032
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,200
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2058 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neocallimastix patriciarum
; STRAIN: 27
; IMMEDIATE SOURCE:
; LIBRARY: genomic DNA library
; CLONE: pNspX-06
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 301..1755
; US-09-390-200-1

Query Match          9.1%; Score 74.2; DB 3; Length 2058;
Best Local Similarity 54.7%; Pred. No. 5.1e-05;
Matches 168; Conservative 0; Mismatches 138; Indels 1; Gaps 1;

QY 185 TGTTAAGATTAATGTTAATGGGATTAATTTCTAGTATTAATGTTGGAAAGTT 244
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Db 1747 TGTCAAAATATAATGATTAGAAATCATTAACCAACCATATTTATTTGTAGATTAAAT 1806
QY 245 AATATATATATATTCATCCCTGTTTATTTTATTTTATTAACACAAATTAATAAT 304
1807 AATTAAGAAAAAATAAATTTTATTTTATTTTATTTTCTCCCTCAATTAATAA 1866
QY 305 TTATTTAACTTTGGTTGTTTTCATTTATGACGGTTAATATTAGTTTAATTAATGAGC 364
Db 1867 TCATTAATAATAGATCATTAATATATTAATTAATTTTTCATTTTATTTTAAATTAATA 1926
QY 365 ATTATTTATATATTAATAATAATATCATGTAATATATGTAAAAAATAATTTAAATATA 424
Db 1927 CGTAAATGTAAATGTAAATTTTAAACAATTTATTTAATATTAAATTTAATAAAGAT-A 1985
QY 425 ATTATTTAATATATATTAATAAACTCAATCAACAATAAAGATAAATTAATCTTAATA 484
Db 1986 CTATTTTAATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2045
QY 485 TATAAAT 491
Db 2046 TATTAAT 2052

RESULT 14

US-09-641-638-651

/ Sequence 651, Application US/09641638

/ Patent No. 6432648

/ GENERAL INFORMATION:

/ APPLICANT: Blumenfeld, Marta

/ APPLICANT: Bougueleret, Lydie

/ APPLICANT: Chumakov, Ilya

/ APPLICANT: Cohen, Annick

/ TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

/ TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

/ FILE REFERENCE: GENSET.051CPI

/ CURRENT APPLICATION NUMBER: US/09/641,638

/ CURRENT FILING DATE: 2000-08-16

/ PRIOR APPLICATION NUMBER: US 09/502,330

/ PRIOR FILING DATE: 2000-02-11

/ PRIOR APPLICATION NUMBER: US 60/133,200

/ PRIOR FILING DATE: 1999-05-07

/ PRIOR APPLICATION NUMBER: US 09/275,267

/ PRIOR FILING DATE: 1999-03-23

/ PRIOR APPLICATION NUMBER: US 60/119,917

/ PRIOR FILING DATE: 1999-02-12

/ NUMBER OF SEQ ID NOS: 1304

/ SOFTWARE: Patent.pm

/ SEQ ID NO 651

/ LENGTH: 20674

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY: misc feature

/ LOCATION: 1123..3123

/ OTHER INFORMATION: 5'regulatory region

/ NAME/KEY: exon

/ LOCATION: 3124..3297

/ OTHER INFORMATION: exon 1

/ NAME/KEY: exon

/ LOCATION: 3871..4072

/ OTHER INFORMATION: exon 2

/ NAME/KEY: exon

/ LOCATION: 5552..5633

/ OTHER INFORMATION: exon 3

/ NAME/KEY: exon

/ LOCATION: 5758..5880

/ OTHER INFORMATION: exon 4

/ NAME/KEY: exon

/ LOCATION: 5936..6099

/ OTHER INFORMATION: exon 5

/ NAME/KEY: exon

/ LOCATION: 6349..6509

/ OTHER INFORMATION: exon 6

NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTGA or TTTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele

[illegible]

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? OTHER INFORMATION: 10-507-321 : polymorphic base A or C
? NAME/KEY: allele
? LOCATION: 13524
? OTHER INFORMATION: 10-507-353 : polymorphic base C or T
? NAME/KEY: allele
? LOCATION: 13535
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Query Match	9.0%;	Score 73.8;	DB 4;	Length 20674;
Best Local Similarity	52.1%;	Pred. No. 7.3e-05;		
Matches: 165; Conservative	0;	Mismatches 152;	Indels 0;	Gaps 0;

OY 196 AATGTTATTGGGAATTACTAATTCTAGTATTAAATGTGCGTTTGGAAGTTAATAATAATT 255
||| ||| ||| ||| ||| ||| |||
Db 11207 AATTAAATTTAATTTTAAATAACATTTAAATTTTTTAATTTAATATAATTAATTAATTTA 11266

256 ATTCATCCTGTTTTTATTTTTTTTATACACAAATTAACAATAATTTATTTAACTT 315

Db 11267 ATTTAATTAATTTAACTTAATTTAATTTAATATTTAATTTAACTTAATTTAATTTAATTT 11326

316 TGGTGGTTTCATTATGACGGTTAATAATTTAGTTAAATAATTGACATTATTATAA 375

Db
11327 AATATTAAATTCTTAATAATTTTAAATTTAATAATTAAATTAAATTAA 11386

376 TTAATAATAATCATTTGTAATATGTAATAATTTAAATTTATTAA7A 435

Db 11387 ATATTAAATTAAATTTTAAATTTGCTCAATATTAATAATTTPAATATT 11446

QY 436 TATATATAAACTCAATCAAAACAATAAAAGATPATTAATTCCTTAATATATATAAATTTT 495

Db
11447 TTATTTAAATAAATTAAAATTAAATTTAAATATTAAATTAAATT 11506

QY 496 TAAATAGCTTTTCACT 512

Db 11507 TAAATTTAATATAAT 11523

RESULT 15

US-10-204-708-10
; Sequence 10, Application US/10204708

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; Patent NO. 661131  
; GENERAL INFORMATION:  
; NAME OF THE INVENTOR
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? APPLICANT: UOEN, Alexander
?
? APPLICANT: PIEPENROCK, Christian
?
? APPLICANT: BEBLIN, Kurt

```

1 AFFILIATION: DEBILIN, AVALC
2
3 TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
4
5 TITLE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204.708

PRIOR APPLICATION NUMBER: PCT/EP01/03971
CURRENT FILING DATE: 2003-05-06

PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8

; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
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; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
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; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98

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; SEQ ID NO 10
;
; LENGTH: 6070
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; TYPE: DNA

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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
ITS-10-204-708-10

Query Match 9.0%; Score 73.6; DB 4; Length 6070;

Best Local Similarity	48.0%;	Pred. No. 7.2e-05;
Matches	241; Conservative	0; Mismatches 259; Indels 2; Gaps 1;

230 TGTGTTGGAAGTTAATAATAATTAATTCATCCTGTTTTTTTAAATTTTAAAC 289

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 20:34:55 ; Search time 3462 Seconds
(without alignments)
10216.036 Million cell updates/sec

Title: US-10-089-557-2_COPY_1_816
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Sequence: 1 actataggcgcgcgtgtgc.....tatttcagtattgttaaag 816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	816	100.0	3041	6	AX370648	AX370648 Sequence
2	124.6	15.3	8056	6	AX599046	AX599046 Sequence
3	123	15.1	8056	6	AX598900	AX598900 Sequence
4	113	13.8	76568	3	MBREV	AF538053 Monosiga
5	107.4	13.2	110000	2	PFMAL8P1_06	Continuation (7 of
6	105.2	12.9	96799	9	AC104647	AC104647 Homo sapi
7	105.2	12.9	250029	3	AE014839	AE014839 Plasmodiu
8	104.8	12.8	85779	8	SCE011856	Av011856 Saccharom
9	104.4	12.8	47972	2	HSBA374F1	AL04592 Homo sapi
10	103.2	12.6	8056	6	AX599046	AX599046 Sequence
11	103.2	12.6	185596	9	AC021553	AC021553 Homo sapi
12	102.6	12.6	2009	6	AX457067	AX457067 Sequence
13	102.2	12.5	67970	3	PFMAL1P3	AL031746 Plasmodiu
14	102.2	12.5	249995	3	AE014840	AE014840 Plasmodiu
15	101.8	12.5	245802	2	AC006279	AC006279 Plasmodiu
16	101.8	12.5	260929	3	AE014852	AE014852 Plasmodiu
17	101.4	12.4	726	3	AB084758	AB084758 Drosophi1
18	100.8	12.4	76568	3	MBREV	AF538053 Monosiga
19	100.8	12.4	114276	9	AC011355	AC011355 Homo sapi
20	100.8	12.4	166706	2	HSBA268E6	AL109803 Homo sapi
21	100.6	12.3	104992	2	AC005504	AC005504 Plasmodiu
22	100.6	12.3	169546	2	AC004157	AC004157 Plasmodiu
23	100.6	12.3	250421	3	AE014849	AE014849 Plasmodiu
24	100.4	12.3	246611	2	AC111404	AC111404 Rattus no
25	100.2	12.3	51552	2	PFMAL7P1_13	Continuation (14 o
26	99.4	12.2	146570	3	AC117072	AC117072 Dictyoste
27	99.2	12.2	25568	3	AC116955	AC116955 Dictyoste
28	99	12.1	340552	3	PEA929354	AL929354 Plasmodiu
29	98.8	12.1	86826	3	PFMAL3P5	AL034556 Plasmodiu
30	98.6	12.1	1496	3	CEY53C12D	AL033123 Caenorhab
31	97.8	12.0	8056	6	AX598900	AX598900 Sequence
32	97.8	12.0	124635	9	AP000593	AP000593 Homo sapi
33	97.6	12.0	53932	2	AC023371	AC023371 Homo sapi
34	97.6	12.0	175544	2	AC117342	AC117342 Rattus no
35	97.4	11.9	141701	2	AL671435	AL671435 Homo sapi
36	97.4	11.9	160401	9	AC009277	AC009277 Homo sapi
37	97.2	11.9	185596	9	AC021553	AC021553 Homo sapi
38	97.2	11.9	258658	3	AE014832	AE014832 Plasmodiu
39	97	11.9	1496	3	CEY53C12D	AL033123 Caenorhab
40	97	11.9	8275	8	AY075133	AY075133 Glycine m
41	97	11.9	8310	6	BD244527	BD244527 Seed coat
42	97	11.9	203162	2	BX890546	BX890546 Danio rer
43	97	11.9	258658	3	AE014832	AE014832 Plasmodiu
44	96.8	11.9	144493	9	AP001547	AP001547 Homo sapi
45	96.8	11.9	181792	9	AC098822	AC098822 Homo sapi

ALIGNMENTS

RESULT 1
AX370648
LOCUS AX370648 3041 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 2 from Patent WO0210413.
ACCESSION AX370648
VERSION AX370648.1 GI:19168813
KEYWORDS
SOURCE Arabidopsis sp.
ORGANISM Arabidopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Li,X., Cai,L., Cheng,N. and Liu,J.W.
Isolation and characterization of a fiber-specific actin promoter

JOURNAL from cotton
Patent: WO 0210413-A 2 07-FEB-2002;
Institute of Molecular Agrobiolology (SG)
FEATURES location/Qualifiers
source 1..3041

ORIGIN

Query Match	100.0%;	Score 816;	DB 6;	Length 3041;
Best Local Similarity	100.0%;	Pred. No. 1.4e-88;		
Matches 816;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ACTATAGGGCACGCGTGTGCGACGGCCCGGCGTGTCTCCTTAAGACAAATTGTGTCAAG	60
Db	1	ACTATAGGGCACGCGTGTGCGACGGCCCGGCGTGTCTCCTTAAGACAAATTGTGTCAAG	60
QY	61	TGCTTCTTCCGAGCAAAATCCGAATAGAGACTTAGAGTAAACATCTAACAGACGCACTGCT	120
Db	61	TGCTTCTTCCGAGCAAAATCCGAATAGAGACTTAGAGTAAACATCTAACAGACGCACTGCT	120
QY	121	CCAGCATTAACCTGTTGGTGA AAAATGTTAATGTAAGTGTCTATGTGCAAGTATTTTCATGG	180
Db	121	CCAGCATTAACCTGTTGGTGA AAAATGTTAATGTAAGTGTCTATGTGCAAGTATTTTCATGG	180
QY	181	AAGGTGTTAAGAATTAAATGTTAATGCGATTAATAATTTCTAGTATTAATTGTGGTTGGA	240
Db	181	AAGGTGTTAAGAATTAAATGTTAATGCGATTAATAATTTCTAGTATTAATTGTGGTTGGA	240
QY	241	AGTTAATATATATTAATTATTCAAATCCTGTTTTTTTATTTTTTTTATTAACACAATTACAA	300
Db	241	AGTTAATATATATTAATTATTCAAATCCTGTTTTTTTATTTTTTTTATTAACACAATTACAA	300
QY	301	TAATTTATTTAACTTTGGTGTGTTTCAATTTATGACGGTTAATATTTTATGTTTAATAAT	360
Db	301	TAATTTATTTAACTTTGGTGTGTTTCAATTTATGACGGTTAATATTTTATGTTTAATAAT	360
QY	361	GAGCATTATATATATTAAATTAATAATCAATGTTGTAATATATGTAAAAATTAATTAAT	420
Db	361	GAGCATTATATATATTAAATTAATAATCAATGTTGTAATATATGTAAAAATTAATTAAT	420
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RESULT 2
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LOCUS	AX599046	8056 bp	DNA	linear	PAT 14-FEB-2003
DEFINITION	Sequence 386 from Patent WO02077272.				
ACCESSION	AX599046				
VERSION	AX599046.1	GI:28399186			
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				

ORIGIN

Query Match	15.3%;	Score 124.6;	DB 6;	Length 8056;
Best Local Similarity	53.3%;	Pred. No. 2.2e-06;		
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OY	189	AAGAATTAAGTTATTGGGATTACTAATTCAGTATTAATGTGTTGGAGCTTAATA	248
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OY	249	TATAATTAATCCAATCCCTGTTTTTATTTTTTTTTTAACACAATTCAAAATTAAT	308
Dd	1706	TAATATTAATAATATATATTTATTAATTTTAATTAATTTAAAATAATAAAAATTTT	1765
OY	309	TTAACCTTGSGTTGTTTCCAATTTATGCGGT-TAATATTTAGTTTAATTAATGACATT	367
Dd	1766	TTAAATTAATAAAATTTAAAAATTAATTAATGTTATATATTTPAATTTAATTAATAAATA	1825
OY	368	ATTATATATTAATAATAATCAATCATTGTAATATATGTAAAAATTAATTTAAATAT	427
Dd	1826	ATTGTGTTTAAAAAATAAAAAAAAAAAAAAAAAATTAATTTAATTAATTAATTTTAT	1885
OY	428	TATTAATATATATTAATAAACTCAATCAAACAATAAAAAAGATAATAATCTTAATA	487
Dd	1886	TTTTTATTAATAAAAAATTAATAATTTTAAAAAATAAATTAATTAATAATAATAAT	1945
OY	488	AAATTTTTTAAAAATAGCTTTTCAGTAAATCTGTCAACAATAGAAAAATTTTTGCAGG	547
Dd	1946	AAAAAATAATTAATTTTTTAAAAATAAATAATTAATATTAATTTTATTAATAATTAATA	2005
OY	548	TTCAATCCAAACACCAGAAAAAGTAATTCATTTTCAGAAAAAGTAATCATTTTCAGAAATT	607
Dd	2006	AAATTTTAAATATATTTTAAATAAATAATATATTTTAAATATTTTAAATTTTAAAAAATT	2065
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Dd	2066	TTATTAATAAAATATTTTAAATATTAATAATAATAATTAATAATTTTAAATTTTAA	2125
OY	668	TTTATTTTCTATTTAGAGAACTAGAAATTGATTTGTCAATGCTTTAATCTA	722
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RESULT 3			
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LOCUS	8056 bp	DNA	linear
DEFINITION	Sequence 240 from Patent WO02077272.		PAT 14-FEB-2003
ACCESSION	AX598900		
VERSION	AX598900.1	GI:28399038	
KEYWORDS	.		

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
synthetic construct	synthetic construct	1	Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.	Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders	Patent: WO 0207272-A 240 03-OCT-2002;	Location/Qualifiers 1. .8056 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="chemically treated genomic DNA (Homo sapiens)"	
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QY	189	AAGAATTAAATGTTATTTGGGATTACTAATTTCTAGATTAATTTGTGTTGGAAGTTAATA	248				
Db	1646	AAAAATTAATTTTAATTAATACGATAAAATTTTATTTTAAATTAATAATTAATAATTTAAT	1705				
QY	249	TATAATTAATCAATCCTGTTTATTTTATTTTATTTTATTAACAACAATTAACAATAATTAAT	308				
Db	1706	TAAATTAATAATTAATTAATTAATTAATTTAATTTAATTAATAATAATAATAATAATTTT	1765				
QY	309	TTAAGTTGGTGGTTTTCATTTATGACGGT-TAATAATTTAGTTTAATTAATGACATT	367				
Db	1766	TTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA	1825				
QY	368	ATTATATATTAATAATAATAATCATTTGTAATATATGTAATAATAATTTAAATAATAATTT	427				
Db	1826	ATTTGTTTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	1885				
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QY	608	ATTTTTCGGAATTTATTTTACTGGCAACAATGAGTCTAAGTGTTCGTTTCTAATTTT	667				
Db	2066	TTATTAATAATAATTTTAAATAATAATAATAATAATAATAATAATAATAATAATAATA	2125				
QY	668	TTTATTTTCTAATTAAGAAACTAGAATTTGATTTGTCAAATGCTTTAATCTA	722				
Db	2126	TAAATTTTCTAATTTAATAATAATAATAATAATAATAATAATAATAATAATAATTTTA	2180				
RESULT 4							
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DEFINITION	Monosiga brevicollis mitochondrion, complete genome.						
ACCESSION	AF538053 AF275274						
VERSION	AF538053.1 GI:23344058						
KEYWORDS	mitochondrion Monosiga brevicollis						
SOURCE	Monosiga brevicollis						
ORGANISM	Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.						
REFERENCE	Butlerwell, C F, Burger, G, and Lang, R F						
AUTHORS	1 (bases 64800 to 65249)						

TITLE	A novel motif for identifying rps3 homologs in fungal mitochondrial genomes
JOURNAL	Trends Biochem. Sci. 25 (8), 363-365 (2000)
MEDLINE	20377911
PUBMED	10916154
REFERENCE	2 (bases 1 to 76568)
AUTHORS	Lang, B.F., O'Kelly, C., Nérard, T., Gray, M.W. and Burger, G.
TITLE	The closest unicellular relatives of animals
JOURNAL	Curr. Biol. 12 (20), 1773-1778 (2002)
MEDLINE	22288938
PUBMED	12401173
REFERENCE	3 (bases 64800 to 65249)
AUTHORS	Lang, F.B. and Bullerwell, C.
TITLE	Direct Submission
JOURNAL	Submitted (06-JUN-2000) Biochimie, Université de Montréal, 2900 Boul. Édouard Montpetit, Montréal, QUE H3C 3J7, Canada
REFERENCE	4 (bases 1 to 76568)
AUTHORS	Burger, G. and Lang, B.F.
TITLE	Direct Submission
JOURNAL	Submitted (10-AUG-2002) Biochimie, Université de Montréal, 2900, Boul. Édouard-Montpetit, Montréal, Québec H3T 1J4, Canada
COMMENT	On Sep 29, 2002 this sequence version replaced gi:9966505.
FEATURES	Location/Qualifiers

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenio, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-680J17; the clone sequenced to the right is RP11-416E16, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-38D12; actual end is at base position 78181 of RP11-416E16.

Data from AC087413 was used to finish this clone, AC104647.

Polymorphisms have been identified between AC098677 and AC104647.

FEATURES
The sequence of AC012566 has been incorporated into AC104647.
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RESULT 7
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REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL
1	Foury, F., Roganti, T., Lecrenier, N. and Purnelle, B.	The complete sequence of the mitochondrial genome of <i>Saccharomyces cerevisiae</i>	FEBS Lett.	440 (3), 325-331 (1998)					
2	(bases 1 to 85779)								
	MIPS.								
	Submitted (16-DEC-1998)	Data collected by MIPS on behalf of the European yeast mitochondrial genome sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, Germany; E-mail: Mewes@mips.biochem.mpg.de							
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Matches 287; Conservative	0; Mismatches 267; Indels 2; Gaps 2;
QY 188	TAAGATTAATGTTATTGGGATTACTAATTTCTAGTATTATTTGTGGTTTGAAGTTAAT 247
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Db 71635	TTATATTATGATATAITTTATTGATATTATTTAATTTAAGATTATTCATTAAATATATA 71694
QY 308	TTTAACCTTGGTTGTTTCAATTATGACGGTTAATATTTTAGTTTAATTAATTGAGCATT 367
Db 71695	ATTATTAAATTTAATATATATTTTAAATTTTATTATATTTTTAAGTAAAGAAACTAT 71754
QY 368	ATTATATATTAATAATAAATCATTTGTAATATATGTAATAAATTAATTAATAATTAAT 426
Db 71755	TTTATATATTTATATATATATATATTAATTTTATAAATGATAAATTTTATATATTATA 71814
QY 427	TTATTAATATATATATAAATCAATCAACAATAAAAAGATATAAATTTCTTAATATATA 486
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	Matches 253;	Conservative	0;	Mismatches 208;	Indels 5;	Gaps 2;
QY	161	ATGTCGAAGTATTTCATCGAAGGTGTTAAACAATTAATGTTATWGGATTACTAATTTCT	220			
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QY	221	AGTATTAATTGTGTTGGAAAGTTAATATATAAATTAATCCATCCTGTTTTTATTTTTT	280			
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QY	341	AATATTTTAGTTTAATAATTGACATTATTATATAATTAATAATAATCAATGTGAATAT	400			
Db	155319	AATATTTTAAAAATATATTAAATAATTTTAAAAATAAAAATATTTTAAAAATATATTTAAAAAT	155378			
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QY	461	AAAAAGATATAAATTCCTAAATATAATAAATTTTAAAAATAGCTTTTGAGTAATCTGT	520			
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QY	521	CATAACAATGAAAAATATTTTTGCAGGTTTCATCCAACACACGAAAGAATGAATCATTTTC	580			

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RESULT 12					
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DEFINITION	Sequence 28 from Patent WO0231186.				
ACCESSION	AX457067				
VERSION	AX457067.1	GI:21715849			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Berlin, K.				
TITLE	Method for the detection of cytosine methylations				
JOURNAL	Patent: WO 0231186-A 28 18-APR-2002;				
	Epigenomics AG (DE)				
FEATURES	Location/Qualifiers				
source	1..2009				

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        JOURNAL
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        EpiGenomics AG (DE)
        Location/Qualifiers
            1..2009
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ORIGIN

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Best Local Similarity	49.4%;	Pred. No. 0.0013;		
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QY	194	TTAATGTTATTTGGGATTACTAATTTCTAGTATTAATTTGGTTGGAAGTTAATATATAA	253	
DB	689	TAAATAAATAATATATATATTATTTAATTTTAAATAACATAAATTTAATTTTAA	630	
QY	254	TTATTCATCCCTGTTTATTTTATTTTATTAACAACAATTAACAATAATTTAATTTAAC	313	
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QY	314	TTTGGTGTTCATTTTCAATTTATGACGGTTAATATTTTACTTTAATATTTGAGCATTATTATA	373	
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QY	614	CGGAATTTATTTTACTGGCAACAATAATGAGCTAAGTGTTCGTTTATTTTATTTTATTT	673	
DB	272	TTTATTTTATTTTATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTT	213	
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Db 212 TTTTATTAAATAACAATATTATATATTTTATTATAAATTATTATT 156

RESULT 13
PFMAL1P3/c

LOCUS PFMAL1P3 67970 bp DNA linear INV 29-JAN-2003

DEFINITION Plasmodium falciparum DNA from MAL1P3.

ACCESSION AL031746 AL844501

VERSION AL031746.9 GI:6594243

KEYWORDS

SOURCE Plasmodium falciparum 3D7

ORGANISM Plasmodium falciparum 3D7

REFERENCE 1 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

AUTHORS Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D., Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K., Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C., Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C., Cronin,A., Davies,R., Davis,P., Dear,P., Dearden,F., Doggett,J., Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N., Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S., Horrocks,P., Humphray,S., Jagels,K., James,K.D., Johnson,D., Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larke,N., Lawson,D., Lennard,N., Line,A., Maddison,M., McLean,J., Mooney,P., Moule,S., Murphy,L., Oliver,K., Ormond,D., Price,C., Quail,M.A., Rabinowitsch,E., Rajandream,M.A., Rutter,S., Rutherford,K.M., Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R., Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L., Whitehead,S., Woodward,J., Sulston,J.E., Craig,A., Newbold,C. and Barrell,B.G.

TITLE Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13

JOURNAL Nature 419 (6906), 527-531 (2002)

MEDLINE 22255708

PUBMED 12368867

REFERENCE 2

AUTHORS Murphy,L., Pain,A., Berriman,M., Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M., Rajandream,M., Hall,N. and Barrell,B.

TITLE Direct Submission

JOURNAL Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

COMMENT On Dec 16, 1999 this sequence version replaced gi:5763807. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.

FEATURES

source 1..67970

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mol_type="genomic DNA"

isolate="3D7"

db_xref="taxon:36329"

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note="synonym: MAL1P3.01b"

complement(join(201..257,455..586,748..804))

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note="synonym: MAL1P3.01b"

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CDS

2990..3276)

gene="PFA0580C"

note="synonym: MAL1P3.01"

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gene="PFA0580C"

note="Originally annotated as Plasmodium falciparum; conserved hypothetical protein but pfam match and other evidences suggest that it is a putative deoxyribonuclease; earlier start site possible to make a 412 aa protein Pfam match to entry PF01026 TatD DNase, TatD related DNase, score 117.30, E-value 2.9e-31

similar to Plasmodium falciparum conserved hypothetical protein, upf0006 family mal1p3.01 SMALL:Q9U0N6 (EMBL:AL031746) (412 aa) fasta scores: E(): 3.7e-150, 100% id in 412 aa, and to Saccharomyces cerevisiae putative deoxyribonuclease yb1055c yb1055c or yb10512 or yb10511 SMALL:YBF5_YEAST (SWALL:P34220) (418 aa) fasta scores: E(): 2.5e-19, 30.47% id in 397 aa"

codon_start=1

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protein_id="CAD49076.1"

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gene="MAL1P3.02"

note="synonym: PFA0585W"

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note="contains possible signal sequence. Signal peptide predicted SignalP 2.0 HMM (Signal peptide probability 0.640, signal anchor probability 0.357) with cleavage site probability 0.504 between residues 27 and 28. ScanRegExp hit to P500867, Carbamoyl-phosphate synthase subdomain signature 2"

codon_start=1

product="hypothetical protein"

protein_id="CAB63557.1"

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db_xref="GOA:Q9U0N5"

db_xref="SPTREMBL:Q9U0N5"

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note="Putative centromere"

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gene="MAL1P3.03"

note="synonym: PFA0590W"

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note="Putative ABC transporter

Pfam match to entry PF00005 ABC tran, ABC transporter, score 45.00, E-value 1.7e-09; HMMsmart hit to SM00382, ATPases associated with a variety of cellular activities; ScanRegExp hit to P500211, ABC transporters family signature

similar to Schizosaccharomyces pombe ATP-binding cassette transporter abc1 abc1 or spac9e9.12C SMALL:ABC1_SCHPO (SWALL:Q92337) (1427 aa) fasta scores: E(): 4.2e-08, 21.46% id in 1146 aa"

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misc_feature

gene

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Db 8535 TTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8476

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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Gardner,M.J., Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W.,
Carlton,J.M., Pain,A., Nelson,K.E., Bowman,S., Paulsen,I.T.,
James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A.,
Kyes,S., Chan,M.-S., Nene,V., Shallow,S.J., Suh,B., Peterson,J.,
Angiuoli,S., Pertea,M., Allen,J., Selengut,J., Haft,D.,
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Fraunholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.I.,
Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C.,
Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and
Barrell,B.
Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
12368864
2 (bases 1 to 249995)
Gardner,M.J.
Direct Submission
Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
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Job time : 3467 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 19:55:10 ; Search time 2676 Seconds

(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers


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TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT      Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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              location/Qualifiers
              1. 1201
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DH007YF12"
              /tissue_type="T CELLS (JURKAT CELL LINE)"
              /cell_line="JURKAT CELL LINE"
              /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
              /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
              with a NotI-oligo(dT) primer. Five prime end enriched,
              double-strand cDNA was digested with Not I and cloned into
              the Not I and EcoRV sites of the pCMVSPORT 6 vector.
              Library was not normalized."

ORIGIN
Query Match      15.4%; Score 126; DB 13; Length 1201;
Best Local Similarity 43.6%; Pred. No. 8.4e-09;
Matches 239; Conservative 81; Mismatches 219; Indels 9; Gaps 2;

QY 194 TTAATGTTATGGGATTACTAATTTCTAGATTAATTTGTGTTGGAAGTTAATATATA 253
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1201 TTTTAAWATATWTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAW 1142

QY 254 TTATTCATCCCTGTTTATTTTATTTTATTAACACAAATTAATTAATTTAATTAAC 313
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1141 ATWTWTAATAAATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1082

QY 314 TTGTTGTTTCAATTTATGACGGTTAATATTTAGTTTAATTAATGAGCATTTATATA 373
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1081 WTTTWTTTTWTWTTTATATTAATAATAATTTTAAWATTTTAAWATTTTAAWATTTTAAW 1023

QY 374 TATTAATAATAATAATCATTTGTAATATATGTAATAATAATAATAATAATAATAATA 433
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1022 TATTATATATATTTTWTWTTTATATTAATAATAATAATAATAATAATAATAATAATAATA 963

QY 434 TATATATATTAATACTCAATCAACAATAATAATAATAATAATAATAATAATAATAATA 493
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 962 AWTWAAWATTAATAAATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTAA 903

QY 494 TTTAAATAAGCTTTTCAGTAATCTGTCAACAATAGAAATATTTTTCAGAGTTCAATC 553
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 902 AAAAAAATAATAAATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTAA 843

QY 554 CAACACACAGAAAGTAATCATTTTCAGAAAGTAATCAT-----TTTCAGAAA 605
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 842 TAAAAAATAATAAATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTAA 783

QY 606 TTATTTTTCGGAATTTATTTTACCTGGCAACAATGAGTCTAAGTCTTCTGTTTAT 665
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 782 ATATATATATATTAATAAATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWAT 723
```

```
QY 666 TTTTATTTTCTAATTAGAGAACTAGAAATGATTTGTCAAATGCTTTAATCTAGCT 725
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 722 TTTTATTTTCTAATTAGAGAACTAGAAATGATTTGTCAAATGCTTTAATCTAGCT 663

QY 726 TGTTTAGA 733
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 662 GGDWAAAA 655

RESULT 4
AL536104/c 1201 bp mRNA linear EST 31-MAY-2003
LOCUS
DEFINITION  AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION  CS0DF022YC18 5-PRIME, mRNA sequence.
VERSION    AL536104
KEYWORDS   AL536104.2 GI:31260974
SOURCE     EST.
ORGANISM   Homo sapiens (human)
REFERENCE  1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 13, 2001 this sequence version replaced gi:12799597.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DF022B09QPI.
              location/Qualifiers
              1. 1201
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DF022YC18"
              /tissue_type="FETAL BRAIN"
              /dev_stage="fetal"
              /clone_lib="Homo sapiens FETAL BRAIN"
              /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
              was primed with a NotI-oligo(dT) primer. Five prime end
              enriched, double-strand cDNA was digested with Not I and
              cloned into the Not I and EcoRV sites of the pCMVSPORT 6
              vector. Library was not normalized."

ORIGIN
Query Match      14.7%; Score 120.2; DB 9; Length 1201;
Best Local Similarity 38.1%; Pred. No. 5.3e-08;
Matches 185; Conservative 97; Mismatches 203; Indels 0; Gaps 0;

QY 198 TGTATTTGGGATTACTAATTTCTAGATTAATTTGTGTTGGAAGTTAATATATATAT 257
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1115 TTTTATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAA 1056

QY 258 TCAATCCCTGTTTATTTTATTTTAAACACAAATTAATTAATTTAATTTAATTTG 317
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1055 TTAATAAATAATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAA 996

QY 318 GTTGTTCATTTATGACGGTTAATATTTTATGTTAATTAATGACATTAATATATAT 377
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 995 ATTWTWTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTAA 936

QY 378 AAATAATAATCATTTGTAATATATGTAATAATAATAATAATAATAATAATAATAATA 437
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 935 CTAATWATTTWAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTTAAWATTTAA 876

QY 438 TATAATAACTCAATCAACAATAATAATAATAATAATAATAATAATAATAATAATAAT 497
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Db	875	AWAATAAATTTTATWAAAAAATAWWAATATWAAAWTTTWTANTAWAATWAAAAAWTTTAW	816
QY	498	AAATAGCTTTTCAGTAAATCTGTCAACAATAGAAAATATTTTTCAGGTCATCCAAA	557
Db	815	WATTATWATTATATWMAWMAWMAWMAWMAWATWATWWTATTAATATAAAAAATTTTAAATAT	756
QY	558	CACCAGAAAAAGTAAATCATTTTCAGAAAAAGTAAATCATTTTTCAGAAATTATTTTTCGGA	617
Db	755	ATWAAWMAWMTATATATATWMAWMAWMAAATWATTATATATATTTTWTATAAAATAMAWMAAAAT	696
QY	618	AATTATTTTACTGGCAACAATGGAGTCTAAGTGTTCGTGTTTATTTTATTTTTC	677
Db	695	AAAAWMAWATAWMAAATTTTATATAHAAHTTATATAAWMHAAATATAKTTTTTDTTTTTTTTTT	636
QY	678	TATTTT 682	
Db	635	TTTTT 631	

RESULT 5					
LOCUS	BX415058/c				
DEFINITION	BX415058	1056 bp	mRNA	linear	EST 15-MAY-2003
ACCESSION	BX415058	Homo sapiens	THYMUS	Homo sapiens	CDNA clone CS0CAP004YG19
VERSION	BX415058				
KEYWORDS	3-PRIME, mRNA sequence.				
SOURCE	BX415058.1	GI:30767520			
ORGANISM	EST.				
	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1056)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrete@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP004AD10NP1.

FEATURES	Location/Qualifiers
source	1..1056

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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="CS0CAP004YG19"
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/clone Tib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match	14.7%;	Score 119.6;	DB 13;	Length 1056;
Best Local Similarity	37.2%;	Pred. No. 7.1e-08;		
Matches 181;	Conservative 101;	Mismatches 204;	Indels 0;	Gaps 0;

QY	254	TTATTCATCCTGTTTTTTTATTTTTTTTATAACACAATTACAATAATTATTAC	313
		: : : : : :	
Db	952	TTTTTTTTTTTWTTTTTTTTNNAMWWWTTWMAAWTTWTTAAWTTTTTTTTTTWT	893
QY	314	TTTGGTGTTCATTTATGACGCTAAATATTTAGTTTAATAATTGAGCATTAATATA	373
		: : : : : : : : : : : :	
Db	892	WYAAACAATTTTWWTTATAAAAWTTAMAAAATTTTTTTTTTWWTWWWWTTWWWWW	833
QY	374	TATTAATAAATAATCATTTGTAATAATATGTAATAATAATTAAAAATATAATTATTA	433
		: : : : : : : : : : : : : : : : : :	
Db	832	WWWWWWWWWWAAAAAAAAAAAAAAAAHHHHHHHHWWWWAAAAAAAAAAAAWWWWW	773

QY	434	TATATATGAATAA	CTCAATCAAA	CAATAAAAA	AGATAA	TAAATTTCTTAAATATAT	AAAATTT	493
		:	:	:	:	:	:	
Db	772	TTWTANNNNNN	NNAATTTTT	TTTTTTT	WAAAAA	AAAAA	AWTTTTTTTTTTTTTTTTTTTT	713
QY	494	TTTAAAAATAG	CTTTTCAGTAA	ATCTGTCAAA	CAATGA	AAAAATATTTTTTG	CAGTTCA	553
		:	:	:	:	:	:	
Db	712	TTTTTTTTT	WTAMAMAM	MTATMAM	TTTTTTT	WCTWCAYAMA	WATMTWATHWHIAT	653
QY	554	CAAA	CACCAGAAAA	GTAAATCATTTT	CAGAAAA	AGTAAATCATTTTT	CAGAAAA	613
		: :	: :	: :	: :	: :	: :	
Db	652	AMAYATHTAT	AWAAATA	TWTWAA	AAAAA	AAAAA	AAAAA	593
QY	614	CGGAAT	TATTTTACTG	CGCAACAA	ATGGAGTCTA	AGTGTCTGTTTTT	TATTTTTT	673
		:	:	:	:	:	:	
Db	592	TTTTTATATAT	ATTTTTTTTT	TTTTTATAT	MTATAA	MAATATAT	ATMTTTTTTTTTTTTT	533
QY	674	TTTCTATTTAG	AGAAACTAGA	AAATTTGATTTGT	CAAAATGCTTTA	ATCTAGCTTGT	TAGA	733
		:	:	:	:	:	:	
Db	532	TTTTTTTATAT	ATAMMMMM	MMHWAAT	TTTTTTT	TWAAATTTWAT	TAATAAA	473
QY	734	TTAGTT	739					
		:						
Db	472	AAWTTT	467					

RESULT 6	CNS00EVL	LOCUS	DEFINITION
CNS00EVL	1101 bp	DNA	linear
Drosophila melanogaster genome survey sequence T7 end of BAC:			
BACR29B23 of RPCL198 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
			GSS 04-JUN-1999

ACCESSION	AL069706	
VERSION	AL069706.1	GI:4949849
KEYWORDS	GSS.	
SOURCE	Drosophila melanogaster	(fruit fly)
ORGANISM	Drosophila melanogaster	

REFERENCE

1 (bases 1 to 1101)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE	1 (bases 1 to 1101)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUN-1999)	Genoscope - Centre National de Sequencage :

COMMENT

med : www.genoscope.cns.fr/
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the library p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

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1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
/note="end : T7"
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ORIGIN	Query Match	Score	DB	Length
Best Local Similarity	14.5%;	118.6;	29;	1101;
	37.9%;	Pred. No. 9.5e-08;		

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP008BE02QP1.

FEATURES

source

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1. 1200
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP008Y104"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dr) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
```

ORIGIN

Query Match 14.5%; Score 118.4; DB 13; Length 1200;
Best Local Similarity 40.7%; Pred. No. 9.5e-08;
Matches 234; Conservative 75; Mismatches 266; Indels 0; Gaps 0;

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QY 144 ATGTTAATGCTAGTCTATGTCGAAGTATTTTCATGGAAGTGTTAAGAAATTAATGTTAT 203
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 393 WTTTWHMAADCTTAATWTTWHCCATSTTSCCTTTTMAAAATTTBBSSTWATATTTTAT 452

QY 204 TGGATTACTAATTTCTAGTATTAATTTGTTGGAGTTAATATATAATTAATTCATC 263
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 453 TTTTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 512

QY 264 CTGTTTATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 323
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 513 WATAMWMTWMAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 572

QY 324 TTCAATTTAGACGTTAATATTTAGTTAATTAATTAATTAATTAATTAATTAATTAAT 383
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 573 AATWMTTWTWTTTWTWMAAATTTTATTTTWTWTTTATTTTATTAATTAATTAATTAAT 632

QY 384 ATTAATCATTTGTAATATGTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 443
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 633 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 692

QY 444 AAACCTCAATCAACATTAATAAGATAATTAATTAATTAATTAATTAATTAATTAATTA 503
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 693 ATATATATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTA 752

QY 504 CTTTTCAGTAATCTGTCGAACATAGAAAATATTTTTCAGAGTTCATCCAAACACCAG 563
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 753 TATATATATATWCAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 812

QY 564 AAAAGTAATCATTTTCAGAAAAGTAATCATTTTTCAGAAAATTAATTTTCGGAATTTAT 623
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 813 AAWTTTAAAAAATTTTAAATTTTAAATAATTTTAAATAATTTTAAATTTTAAATTTTAA 872

QY 624 TTTACTGCAACAATGAGTCTAAGTCTTCTGTTTATTTTATTTTATTTTATTTTATTTA 683
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 873 TWAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAA 932

QY 684 GAGAACTAGAAATTTGTCGAATGTCTTTAA 718
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 933 TTTWMAAATTAATAATTAATAAATAATTTTWTWMA 967
```

RESULT 9
AL536104 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF022YC18 5-PRIME, mRNA sequence.
ACCESSION AL536104
VERSION AL536104.2 GI:31260974
KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12799597.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF022B09QP1.

FEATURES

source

```
1. 1201
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF022YC18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dr) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
```

ORIGIN

Query Match 14.4%; Score 117.4; DB 9; Length 1201;
Best Local Similarity 37.1%; Pred. No. 1.3e-07;
Matches 194; Conservative 111; Mismatches 217; Indels 1; Gaps 1;

```
QY 193 ATTAATGTTATGGGATTAATTAATTTCTAGTAATTAATTTGTTGGAGTTAATATATA 252
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 666 ATAADTTATATAAATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTA 725

QY 253 ATTATCAATCTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 311
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 726 ATWATTTTWTWATATATATWMTTWTWATATTTTAAATTTTATTAATTTTATTAATTA 785

QY 312 ACTTGTGTTTCTCAATTTATGACGTTAATTTTATTTTATTTTATTTTATTTTATTTTAT 371
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 786 ATWTTTWTWTTTWTWKATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 845

QY 372 TATATTAATTAATAATCATTTGTAATATATGTAATAATTAATTAATTAATTAATTAAT 431
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 846 WATATTWMAATTTTAAATAATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 905

QY 432 AATATATTAATAAATCAATCAACATTAATAAAGATAATAATTAATTTCTTAATATATAAT 491
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 906 AWTTTTAAWMAATTTTAAATAATTTAAATAATTTAAATAATTTAAATAATTTAAATAAT 965

QY 492 TTTTAAATAGCTTTTCAAGTAATCTGTCGAACAATGAATAATTTTTCGAGGTTCGA 551
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 966 AWWMTTAAWMAATTTTAAATAATTTAAATAATTTAAATAATTTAAATAATTTAAATAAT 1025

QY 552 TCCAAACACAGAAAAGTAATCATTTTCAGAAAAGTAATCATTTTTCAGAAAATTAATT 611
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 1026 WATWSTATWATAAATAATTAATTTTAAATAATTTAAATAATTTAAATAATTTAAATAAT 1085

QY 612 TTGGAATTAATTTTACTGCAACAATAAGAGTCTAAGTCTTCTGTTTATTTTATTTTAA 671
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 1086 AAAMWMAWMTATTTTAAATAATTTAAATAATTTAAATAATTTAAATAATTTAAATAAT 1145

QY 672 TTTTCTATTTAGAGAACTAGAAATTTGATTTGTCGAATGTCT 714
   |||::: : |||::: : |||::: : |||::: : |||::: : |||::: : |||::: :
Db 1146 WTTTADAMDATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1188
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RESULT 10
CNS00EVL/c      1101 bp      DNA      linear      GSS 04-JUN-1999
LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC:
                  BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION      AL069706
VERSION
KEYWORDS
SOURCE
ORGANISM        Drosophila melanogaster (fruit fly)
                  Drosophila melanogaster
                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                  BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                  - Web : www.genoscope.cns.fr)
COMMENT        Determination of this BAC-end sequence was carried out as part of a
                  collaboration with the Berkeley Drosophila Genome Project (BDGP).
                  The BDGP is constructing a physical map of the Drosophila
                  melanogaster genome using these BACs. For further information
                  please see http://www.fruitfly.org The BDGP Drosophila
                  melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                  Aaron Mammoler in Pieter de Jong's laboratory in the Department of
                  Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                  NY. The library is named RPCI-98 and was constructed by partial
                  EcoRI digestion of Drosophila DNA provided by the BDGP from the
                  isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
                  p1 and EST libraries. A more detailed description of the library
                  and how to order individual BAC clones, the entire library, or
                  filters for hybridization from the BACPAC Resource Center can be
                  found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source          1. 1101
                  /organism="Drosophila melanogaster"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:7227"
                  /clone="BACR29B23"
                  /clone_lib="RPCI-98"
                  /note="end : T7"
ORIGIN
Query Match    14.2%; Score 116.2; DB 29; Length 1101;
Best Local Similarity 37.7%; Pred. No. 2e-07;
Matches 208; Conservative 107; Mismatches 225; Indels 11; Gaps 1;
QY 190 AGAATTAATGTTAATGGATTACTAATTTCTAGTATTAATTGTTGGAAAGTTAATAT 249
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1006 ATATTAATTAATTAATATATATATAAATAAATAAATAAATAAATAAATAAATAA 947
QY 250 ATTAATTAATCAATCCTGTTTATTTTATTTTATTAACACAAATTAACAATTAATTAT 309
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 946 WAATATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 887
QY 310 TAACTTTGGTTGTTTCAATTTATGACGTTAATATTTTATTAATTAATTAATTAATTA 369
    ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 886 AAWTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 827
QY 370 TATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 429
    ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 826 TWTWTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 767
QY 430 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 489
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 766 TATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 707
QY 490 ATTTTAAAAATAGCTTTTCAGTAAATCTGTCAACAATAGAAAAATATTTTGCAGGTT 549
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 706 WTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 647
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QY 550 CATCCAAACACAGAAAAGTAAATCATTTTCAGAAAAGTAAATCATTTTTCAGAAATTA 609
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Db 646 ATT-----AAATTATTAATAATAATAATAATAATAATAATAATAATAATAATA 598
QY 610 TTTTCGAAATTAATTTTACTGCGCAACAATAAGAGTCTAAGTGTCTGTTTATTTT 669
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 597 ATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 538
QY 670 TATTTTCTATTTAGAGAACTAGAAATTTGATTTGTCAAATGCTTAAATCTAGCTTGT 729
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 537 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 478
QY 730 TAGATTAGTTG 740
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Db 477 WAAATTWKKK 467
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RESULT 11
CNS0167M      1201 bp      DNA      linear      GSS 26-JUL-1999
LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
                  BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION      AL106396
VERSION
KEYWORDS
SOURCE
ORGANISM        Drosophila melanogaster (fruit fly)
                  Drosophila melanogaster
                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
                  BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                  - Web : www.genoscope.cns.fr)
COMMENT        Determination of this BAC-end sequence was carried out as part of a
                  collaboration with the European Drosophila Genome Project (EDGP) -
                  http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
                  library (Dros BAC) was made by Alain Billaud at CERH (Centre
                  d'Etude du Polymorphisme Humain) with funding provided by a MRC
                  project grant. The DNA was prepared from embryos by Alain Bucheton
                  and Genevieve Payan. It has been constructed in the vector
                  pBelOBAC11.
FEATURES
source          1. 1201
                  /organism="Drosophila melanogaster"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:7227"
                  /clone="BACN15M24"
                  /clone_lib="DrosBAC"
                  /plasmid="pBelOBAC11"
                  /note="end : T7"
ORIGIN
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Query Match    14.2%; Score 116; DB 29; Length 1201;
Best Local Similarity 41.6%; Pred. No. 2e-07;
Matches 236; Conservative 70; Mismatches 260; Indels 1; Gaps 1;
QY 127 TTAACGTTTGGTGAATAATGTAATGTAAGTCTATGTCGAAGTAATTTTCATGAAGGTG 186
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 632 TTTANGCTTTAKKKTGTTTBTBTTKTTTGTGKKKKKTKTKTTGTTGDAAAAAA 691
QY 187 TTAAGAAATTAATGTTATGGGATTAATAATTTCTAGTATTAATTTGTTGGAAGTTAA 246
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 692 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 751
QY 247 TATATAATTAATCAATCCTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 305
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 752 WTTTATTTTAAWATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 811
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 20:51:30 ; Search time 472 Seconds

(without alignments)
8726.094 Million cell updates/sec

Title: US-10-089-557-2_COPY_1_816

Perfect score: 816
Sequence: 1 actataggcgcgcgtgtgc.....tatttcagtattgtaaaag 816

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	124.2	15.2	606	17	US-10-021-323-7696	Sequence 7696, Ap
2	92.6	11.3	520	17	US-10-021-323-7699	Sequence 7699, Ap
3	92.4	11.3	3673778	15	US-10-312-841-1	Sequence 1, Appl
4	90.6	11.1	469	17	US-10-021-323-16830	Sequence 16830, A
5	90.2	11.1	7351	15	US-10-311-455-2	Sequence 2, Appl
6	90.2	11.1	8305	15	US-10-311-455-1542	Sequence 1542, Ap
7	89.8	11.0	18357	17	US-10-433-793-114	Sequence 114, App
8	89.4	11.0	6106	13	US-10-221-714A-151	Sequence 151, App
9	89.4	11.0	6106	15	US-10-311-455-1445	Sequence 1445, Ap
10	89.4	11.0	6106	17	US-10-257-166-113	Sequence 113, App
11	89.4	11.0	158001	17	US-10-211-179-11	GENERAL INFORMATI
12	89.2	10.9	565	17	US-10-021-323-11125	Sequence 11125, A
13	88.8	10.9	520	17	US-10-021-323-7699	Sequence 7699, Ap
14	88.2	10.8	560	17	US-10-021-323-2253	Sequence 2253, Ap

15	88.2	10.8	16602	15	US-10-311-455-700	Sequence 700, App
16	87.8	10.8	419	9	US-09-960-352-11234	Sequence 11234, A
17	87.4	10.7	17848	15	US-10-239-676-28	Sequence 28, Appl
18	87.4	10.7	17848	15	US-10-240-453-38	Sequence 38, Appl
19	87.4	10.7	17848	17	US-10-257-166-58	Sequence 58, Appl
20	87.2	10.7	15548	15	US-10-311-455-2128	Sequence 2128, Ap
21	86.6	10.6	158001	17	US-10-211-179-11	GENERAL INFORMATI
22	86	10.5	38342	13	US-10-221-714A-472	Sequence 472, App
23	85.8	10.5	469	17	US-10-021-323-16830	Sequence 16830, A
24	85.8	10.5	5487	15	US-10-311-455-1571	Sequence 1571, Ap
25	85.2	10.4	543	17	US-10-021-323-12208	Sequence 12208, A
26	85.2	10.4	6465	15	US-10-311-455-958	Sequence 958, App
27	85	10.4	3673778	15	US-10-312-841-2	Sequence 2, Appl
28	84.8	10.4	5845	15	US-10-311-455-1636	Sequence 1636, Ap
29	84.6	10.4	27890	17	US-10-741-601-5686	Sequence 5686, Ap
30	84.6	10.4	126872	17	US-10-741-601-5738	Sequence 5738, Ap
31	84.4	10.3	6063	13	US-10-221-714A-59	Sequence 59, Appl
32	84.4	10.3	6216	17	US-10-257-166-13	Sequence 13, Appl
33	84.4	10.3	13511	15	US-10-311-455-254	Sequence 254, App
34	84.2	10.3	6478	15	US-10-239-676-124	Sequence 124, App
35	84.2	10.3	6478	15	US-10-240-453-144	Sequence 144, App
36	84.2	10.3	6626	13	US-10-221-714A-536	Sequence 536, App
37	84	10.3	960	15	US-10-198-846-6381	Sequence 6381, Ap
38	84	10.3	6881	15	US-10-311-455-1353	Sequence 1353, Ap
39	84	10.3	6881	15	US-10-240-453-123	Sequence 123, App
40	83.8	10.3	560	17	US-10-021-323-2253	Sequence 2253, App
41	83.6	10.2	7008	13	US-10-221-714A-254	Sequence 254, App
42	83.4	10.2	56153	13	US-10-221-714A-520	Sequence 520, App
43	83.4	10.2	3673778	15	US-10-312-841-2	Sequence 2, Appl
44	83.2	10.2	6106	13	US-10-221-714A-152	Sequence 152, App
45	83.2	10.2	6106	15	US-10-311-455-1446	Sequence 1446, Ap

ALIGNMENTS

RESULT 1
US-10-021-323-7696/c
; Sequence 7696, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Delkman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 7696
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(606)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-019-Q1-N6-D2
US-10-021-323-7696

Query Match 15.2%; Score 124.2; DB 17; Length 606;
Best local Similarity 82.9%; Pred. No. 7.6e-08;
Matches 155; Conservative 0; Mismatches 28; Indels 4; Gaps 1;

QY 186 GTTAAGATTAATGTTATTTGGGATTAATTTCTAGTATTAAATGTTGGAAGTTA 245
|||
Db 183 GTCAAGCATTTCCAGCGTTTATTTTAAATTTCTAGTATTAAATGTTGGAAGCTA 124
QY 246 ATATATAATTAATTCATCTGTTTATTTTATTTTATTTTATTAACAATTAACAATAATT 305


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Db      123 ATTATATATATTCAGTCC-----TTTTTTTATTTTATATATAACACAAATTAATAAT 68
QY      306 TATTTAAGCTTGGTTGTTTTCATTTAAGCGGTTAATATTTAGTTTAATAATTGAGCA 365
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      67 TATTTGGCTTGGTTGTTTTCATTTAATGAACGTTAATATTTCTAGCTTAATAATTGAGTA 8
QY      366 TTATATAT 372
        ||||| |||||
Db      7 TTACTAT 1
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RESULT 2

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US-10-021-323-7699
; Sequence 7699, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 7699
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB828-019-Q1-N6-D6
US-10-021-323-7699
```

Query Match 11.3%; Score 92.6; DB 17; Length 520;
Best Local Similarity 53.1%; Pred. No. 0.0013;
Matches 197; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

```
QY      209 TTACTAATTTCTAGTATTAATTGTGTTGGAAGTTAATATATATATTAATTCATCCTTGT 268
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      13 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 72
QY      269 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 328
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      73 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 132
QY      329 TTTATGACGGTAAATTTTATGTTTAATTAATGAGCATTATATATTAATAATAATAA 388
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      133 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 192
QY      389 TCATTTGTAATATATGTAATAAAATTAATTAATAATAATAATAATAATAATAATAACT 448
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      193 AAAATTAATAAAATTTTAATAAAATTTTAATAAAATTTTAATAAAATTTTAATAAAATTT 252
QY      449 CAATCAAAACAATAAAAGATTAATTAATTTTAATATATATTAATAATAATAATAAGCTTTT 508
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      253 AAAAAAAAAAGTAAATTTTAATAAAATTTTAATAAAATTTTAATAAAATTTTAATAAAAT 312
QY      509 CAGTAAATCTGTCAACAATAGAAATATTTTTCAGGTTTCATCCAAACACCAAGAAAG 568
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      313 AAATTAATTTATTAATAAAATTTTAATAAAATTTTAATAAAATTTTAATAAAATTTTA 372
QY      569 TAAATCATTTT 579
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Db      373 AAAAATAATAT 383
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RESULT 3
US-10-312-841-1
; Sequence 1, Application US/10312841

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; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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Query Match 11.3%; Score 92.4; DB 15; Length 3673778;
Best Local Similarity 48.9%; Pred. No. 0.016;
Matches 275; Conservative 0; Mismatches 286; Indels 1; Gaps 1;

```
QY      145 TGTTAATGGTAGTGTATGTCGAAGTATTTTCATGGAAGGTGTAGAAATTAATGTTAT 204
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205750 TTTTATATTAAGTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 205809
QY      205 GGGATTACAAATTTCTAGTATTAATTTGCGTTTGAAGTTAATATAATAATTATCAATCC 264
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205810 TTTTATATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 205869
QY      265 TTGTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 324
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205870 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 205929
QY      325 TCAATTTAGACGGGTTAATATTTTATTTAGTTTAATAATTGAGCATTATTAATAATAA 384
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205930 TTTTATATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 205989
QY      385 TAAATCATTTAATATATGTAATAAAATTTTAATAATAATAATAATAATAATAATAATA 443
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205990 TTTTACGTATGTTGTTATTTAGTAAGTATTTTGAATTTATATAGTTAAAGTAAATAT 206049
QY      444 AAACCTCAATCAACAATTAATAAAAGATTAATAATCTTAATAATATAATAATTTTAA 503
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      206050 TATGTAATTAAGAAATAAGTAATAATAAGAGTTATTAATAGAGTTGAATAAAATG 206109
QY      504 CTTTTCAGTAATCTGTCAACAATAGAAATATTTTTCAGAGTTTCATCCAAACACACAG 563
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      206110 TTTGTTAATAATTTTGTAGTTAAGATAGCGTTTAAATTTAATTTTAAATTAAGTG 206169
QY      564 AAAAGTAATCAATTTTCAGAAAGTAATCAATTTTTCAGAAATTAATTTTCGAAATTA 623
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Db      206170 TTTAGAATATATGAGTTTAAGTTGATATTAATTTTGGAAATTAATATTAATTA 206229
QY      624 TTTACTGGCAACAATGAGTCTAAGTCTTCTGTTTATTTTATTTTCTAATTTA 683
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      206230 GTATGTTAAAGTTTATATATATATATCGTTTAAATTTTATTTTAAATTAATTA 206289
QY      684 GAGAACTAGAAATGATTTGT 705
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      206290 GCGGTTTCTTTGTTATGTGT 206311
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RESULT 4
US-10-021-323-16830/c
; Sequence 16830, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: Plants
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16830
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-024-Q6-N6-E4
US-10-021-323-16830
```

Query Match 11.1%; Score 90.6; DB 17; Length 469;
Best Local Similarity 54.3%; Pred. No. 0.0023;
Matches 183; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

```
QY 200 TTATTGGATTACTTAATCTCTAGTATTAATGCTTGGAGTAAATTAATTAATTC 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 TTTTATTTTAAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 284

QY 260 AATCCTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 224

QY 320 TGTTCATTTATGACGTTAATATTTTATTTTATTTTATTTTATTTTATTTT 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 164

QY 380 ATAAATAAATCATTTGTAATATATGTAATAATTTTAAATATATTAATTAAT 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 104

QY 440 TAATAAACTCAATCAACAATAAAGATTAATTAATCTTAAATATATTAATTT 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

QY 500 ATAGCTTTCAGTAAATCTGTCAACATAGAAATA 536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
```

RESULT 5

```
US-10-311-455-2
; Sequence 2, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2
; LENGTH: 7351
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2
```

Query Match 11.1%; Score 90.2; DB 15; Length 7351;
Best Local Similarity 49.4%; Pred. No. 0.0056;
Matches 295; Conservative 0; Mismatches 293; Indels 9; Gaps 2;

```
QY 140 GAAATGTTATGCTAGTCTATGTCAGATTTTCATGAGAGTGTAAAGATTAATG 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 897 GATTATTTTATTAATTTTATTTATGATATAAATATTTAGTATTAAGATTTATTA 956

QY 200 TTATTGGATTACTTAATTTCTAGTATTAATTTGCTTTGGAAGTTAATTAATTC 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 957 TTATTTAAAGATATTAATAAAATTTTAAATGCTTTGATATTTAATATTTT 1016

QY 260 AATCCTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1017 TTTTATTTTATTTTGAATTTGAATTTTATGTTAATTTATATATAGAAATTT 1076

QY 320 TGTTCATTTATGACGTTAATATTTTATTTTATTTTATTTTATTTTATTT 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1077 TTTTATTTTATTTTAAATATTTTATTTTATTTTATTTTATTTTATTTTAT 1136

QY 380 ATAAATAAATCATTTGTAATATATGTAATAAATTTAAATATTAATTAATATA 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1137 ATATACGTAAT-----GTATATTTATGTTATATATATATATATATATATA 1189

QY 440 TAATAAACTCAATCAACAATAAAGATTAATTAATTTCTTAATATATTAATTT 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1190 TAATATATATATATATGTAATATATATGTCGGTAGCTAAATTTAATTTT 1249

QY 500 ATAGCTTTCAGTAAATCTGTCAACAATAGAAATATTTTTCAGAGTTCAATCA 559
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 ATAGAAATGTAATTAATAATTTATTAATAATTAATTAATTTTTCAGAGTT 1309

QY 560 CCAGAAAGTAAATCATTTTCAGAAAGTAAATCATTTTTCAGAA--ATTAATTT 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1310 AAAATATTTGTAATTAATTTGATTAATAAATAAATAATTAAGTATGATTA 1369

QY 618 AATTATTTTACGCAACAATAAGAGTTAAGTTCTGTTTATTTTATTTTATTC 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1370 AGATATTAATAATTAATATTTTGAAGTATATTTTATGAGAATGATGAGTTT 1429

QY 678 TATTAGAGAACTAGAAATGATTTGTCAAATGCTTAACTAGCTGTTAGAT 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1430 TTTTATGTAATTTATGATTTTATGATTTGATTTGAATTAAGAAATTAATA 1486
```

RESULT 6

```
US-10-311-455-1542
; Sequence 1542, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1542
; LENGTH: 8305
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1542
```

```
Query Match      11.1%; Score 90.2; DB 15; Length 8305;
Best Local Similarity 50.1%; Pred. No. 0.0058;
Matches 284; Conservative 0; Mismatches 273; Indels 10; Gaps 2;

QY 173 TTTCATGGAAGGTGAAGAATTAATGTTATGGGATTACTAATTTCTAGTATTAATTGT 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1710 TTTTAGTTGGGTAATAAAGTAAGATTGTTTTTTATATATATATATATATACGT 1769

QY 233 GGTGGAGTAAATATATTAATTAATTCATCCCTGTTTATTTTATTTTATTAACACA 292
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1770 ATATACGTATTAATATATATATATATATATATATATATATATATAAATAA 1829

QY 293 ATTACAATAATTAATTAACCTTGGTGTTCATTTATTTATGACGGTAAATTTTAGT 352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1830 ATAATAAATATGTTATTTATTTTAAATGTAATAAATAAATATAATTTATTTAT 1889

QY 353 TAATAATGACATTAATATATTAATAATAATCAATGTAATATATGTAATAA 412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1890 ATATAAATATATATGTTATTAATATATATATTAATATATATTTAATAAGAAATAT 1949

QY 413 TTTAAATATTAATTTATTAATATATATATTAATCAATCAACAAATAAAGATA 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1950 ATTATTAATATTAATTAATATATATATATATATATATATATATTTATTTAT 2003

QY 473 AATCTTAATATATAAATTTTAAATAGCTTTTCAGTAAATCTGCAACAATAGAA 532
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2004 ATATATATATATATAATATATATATATATATATATAATATATATATATATA 2063

QY 533 AATATTTTTCAGGTCATCCAAACACAGAAAGTAATCATTTTCAGAAAAGTAAT 592
    ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 2064 TATATTAT---ATATATTATATATATATATATATTTTATATATATATATATAT 2119

QY 593 CATTTTCAGAAATTAATTTTCGAAATTAATTTTACTGCAACAACAATGAGCTTAAGT 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2120 TATATATATATAATATATATATATTTTATTAATATATATATATATATATATAT 2179

QY 653 TTCTGTTTTTATTTTATTTTCTATTTAGAGAACTAGAAATGATTTGCAATGT 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2180 TATATATTTTATATATATATTTATTAATATGTAATATAATAATAATAATATAT 2239

QY 713 CTTTAATCTAGCTTTAGATTAGT 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2240 ATATTATTAGGAGTTTGAGATTAGT 2266

RESULT 7
US-10-433-793-114
; Sequence 114, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 114
; LENGTH: 18357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-114

Query Match      11.0%; Score 89.8; DB 17; Length 18357;
Best Local Similarity 48.9%; Pred. No. 0.0081;
Matches 302; Conservative 0; Mismatches 307; Indels 8; Gaps 2;

QY 124 GCATTAACTGTTGGTGAATAATGTTAATGCTATGTCGAAGTATTTTCATGGAAG 183
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15286 GTATTAAATTATTATTAGTTTGTAGTAGTTGCGGAGTGTTTTATAGAGATGCT 15345

QY 184 GTGTTAAGATTAATGTTATTGGGATTACTAATTTCTAGTATTAATGTGTTGGAAGT 243
```

```
Db 15346 TTTATTATAAATTAAGATATTATAATTAATAATTTGTTTATGATTTTAAATGAGGT 15405

QY 244 TAATATATAATTATCAATCCTGTTTATTTTATTTTATTAACACAAATTACAATAA 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15406 TTATGTTGGAAGTTTATTTGTTTATTTTGTGTTTGGTATTTAATGTTTGGTATAT 15465

QY 304 TTTATTAACTTTGGTGTGTTTCAATTTATGACGGTAAATTTTATGTTAATAATTAG 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15466 TTTTATTATTTGTTATATATATGAGTTAGTTATTTGTTTGGTTTAATAGTGTGAG 15525

QY 364 CATTAATATATTAATAATAATCAATGTAATATATATGTAATAAATAATTAAATATA 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15526 GTGTTTAAAGAAATTTAAAGAGAAATTCGTAATAATATATATAAATTATTAAGTTA 15585

QY 424 AATTATTAATATATATATATAAATCAATCAACAATAAAGATAATAATCTTAAT 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15586 GATTATTTAAATGTTTTTTATTTTAAATGAGTGAATAATTCGATTAAATTTTATATAT 15645

QY 484 ATATAAATTTTAAATAGCTTTTCAGTAAATCTGCAACAATAAGAAATATTTTGTG 543
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15646 AATATAGT-----AATAGATAGAAATAAATAATATATATATATATATGTAATTTAT 15698

QY 544 CAGGTCATCCAAACACCAAGAAAGTAATCATTTTCAGAAAAGTAATCATTTTTCAGA 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15699 TATGTTAATTTAATAGAGAGATTGTAGGTTTATTTGTATAGTAATTTTATTTAT 15758

QY 604 AATTATTTTTCGAAATTAATTTTACTGCAACAATAAT-GGAGTCAAGTGTCTGTTT 662
    ||||| | | | | | | | | | | | | | | | | | | | | |
Db 15759 TTTTATGTTTTTTAAATTTTATTTTATTTAATTAAGTTTAAAGTTTGTGTT 15818

QY 663 TATTTTATTTTCTATTTAGAGAACTAGAAATGATTTGTCAATGCTTTAATCTA 722
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15819 TATTTTGGTTTTTTTATTTTGTGTTTGTGTTTGTGTTTGTGTTTATTTATTTT 15878

QY 723 GCTGTTTAGATTAGT 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15879 TTTTATTAGTTT 15895

RESULT 8
US-10-221-714A-151
; Sequence 151, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 151
; LENGTH: 6106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-151
```


Query Match	11.0%	Score 89.4;	DB 13;	Length 6106;
Best Local Similarity	51.7%;	Pred. No. 0.0068;		
Matches 278; Conservative	0;	Mismatches 253;	Indels 7;	Gaps 3;

[illegible]

```

RESULT 9
US-10-311-455-1445
; Sequence 1445, Application US/10311455
; Publication No. US20030143606A1
;
GENERAL INFORMATION:
;
APPLICANT: OLEK, Alexander
;
APPLICANT: PIEPENBROCK, Christian
;
APPLICANT: BERLIN, Kurt
;
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Cytosine Methylation of DNA
;
TITLE OF INVENTION: Cytosine methylation
;
FILE REFERENCE: 5013.1014
;
CURRENT APPLICATION NUMBER: US/10/311,455
;
CURRENT FILING DATE: 2002-12-16
;
PRIOR APPLICATION NUMBER: PCT/EP01/07537
;
PRIOR FILING DATE: 2001-07-02
;
PRIOR APPLICATION NUMBER: DE 10032529.7
;
PRIOR FILING DATE: 2000-06-30
;
PRIOR APPLICATION NUMBER: DE 10043826.1
;
PRIOR FILING DATE: 2000-09-01
;
NUMBER OF SEQ ID NOS: 2424
;
SEQ ID NO 1445
;
LENGTH: 6106
;
TYPE: DNA
;
ORGANISM: Artificial Sequence
;
FEATURE:
;
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1445

```

Query Match	11.0%;	Score 89.4;	DB 15;	length 6106;
Best Local Similarity	51.7%;	Pred. No. 0.0068;		
Matches	278;	Conservative	0;	Mismatches 253;
			Indels	7;
			Gaps	3;

QY	198	TGTTATTGGGATPACTAAATTTCTAGATTAATATGTGCTTTGGAACTTAATATTAATTTAT	257
Db	2612	TTTTTAATTTAAATGGTTTTTGTGTTTTTAAAGAGTTAAAGAGAAATTAATTAATAAGTTA	2671
QY	258	TCAATCCCTGTTTTTATTTTTTTTTTAAACAACAATTACAATTAATTAATTTAACTTTG	317
Db	2672	TTAATGTTTAAATTTTAAAGTTTTTTTAAATATTAATTAATATATATTAATATTAATAAGTTA	2731
QY	318	GTTGTTTCAATTTATGACGCGTTAATATTTAGTTTAATTAATTTGAGCATTATTAATATT	377
Db	2732	TATATATAATTAATTAATATATATATAATATTAATTAATGATTAATTAATATTAATAAATT	2791
QY	378	AAATAAATTAATCAATGTAAATATATGTAAAAATAATTTAAATATTAATTAATTAATATA	437
Db	2792	AAATAAATTAATTAATTAATTAATAT -TAAATTAATTAATTAATTAATTAATTAATTAATA	2850
QY	438	TATAATTAACCTCAATCAACAATTAAGATAATAAATCTTAA----ATATAATAAATT	492
Db	2851	TATTAATATATATTAATTAATTAATTTGATTAATTAATTAATTAATTAATTAATAATTA	2910
QY	493	TTTTAAATAGCTTTTCAGTAAATCTGTCAACAATAGAAATATTTTTTGCAGGTTCAAT	552
Db	2911	TTATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATAAT	2970
QY	553	CCAAACACGAGAAAGTAAATCATTTTCAGAAAAGTAAATCATTTTTCAGAAATTAATTTT	612
Db	2971	-TATATATAATTAATTAATAATTAATTAATTAATTAATTAATTAATTAATAAGTTTTTAT	3029
QY	613	TCCGAAATTAATTTTACTGCCAAACAATGGAGCTTAAGTGTCTCTGTTTATTTTTTAT	672
Db	3030	ATATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTATTTT	3089
QY	673	TTTTCTATTTAGAGAAACTAGAAATGCAATGCTTTAATCTAGCTGTGTT	730
Db	3090	TATAGTATTTTAATTAATTAATTTGTGGTTTAAATTTGAGCTTAATGTAATTTGTGTTT	3147

```

RESULT 10
US-10-257-166-113
; Sequence 113, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 113
; LENGTH: 6106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-113

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Query Match	11.0%;	Score 89.4;	DB 17;	Length 6106;
Best Local Similarity	51.7%;	Pred. No. 0.0068;		
Matches	278;	Conservative 0;	Mismatches 253;	Indels 7;
			Gaps	3;
QY	198	TGTTATTGGCAATTACTAATTTCTAGATTAATTTGGTTGGAAGTTATATATAATTAAT	257	
Db	2612	TTTTTATTTTAAATGGTTTTTTGTTGTTTAAAGATTAAAGAGAAATTATTTAAATAAGTTA	26711	

QY	258	TCATCCCTGTTTTTTTATTTTTTTTATTAACACAATTCACAAATTAATTTAACTTTG	317
Db	2672	TTAATGTTTATATTTTGAAGTTTTTTAAATATATATATTAATATATTAATTAAGTTA	2731
QY	318	GTTGTTTCATTTTATGACGGTTAATATTTAGTTTAATTAATTGAGCATTTATATATT	377
Db	2732	TATATATTAATTAATTTATATATATAATTAATTAATTAATTAATTAATTAATTAAT	2791
QY	378	AAATTAATTAATTCATTTGTAATATATGTAATAATTAATTTAAATATTAATTTAATATA	437
Db	2792	AATATTAATTAATTTATATATATTATAT- TAATTAATTTATATATTTAAATATATTAATTAATAA	2850
QY	438	TATTAATTAATTCATTCAAACAATTAATAATTAATTTCTTAA----ATATATAAATT	492
Db	2851	TATTAATTAATTTATATATATTATATTGATTAAATTAATTTATTAATAATTAATTAATAATTA	2910
QY	493	TTTTAAATAGCTTTTCAGTAATCTGTCAACAATAGAAATATTTTTTCAGAGTTTCAT	552
Db	2911	TTATTAATTAATTTATATATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2970
QY	553	CCAAACACGAGAAAGTAATCATTTTCAGAAAAGTAATCATTTTTTCAGAAATTAATTTT	612
Db	2971	-TATATATAATTAATTTATAAATTAATTTATATATAATTAATTAATTAATTAATTAATTAAT	3029
QY	613	TCGGAATTAATTTTACTGGCAACAATGAGTCTAAGTCTTCTGTTTTTATTTTTTAT	672
Db	3030	ATATTAATTAATTTATATATTTTATATATTTATATATAATTAATTTATTTTATTTTAT	3089
QY	673	TTTTCTATTTAGAGAAACTAGAAATGTATTGCAAAATGCTTTAATCTAGCTTGT	730
Db	3090	TATAGTATTTTATATTAATTTTGTGTTTATTTGAGCTTAATTTGATTTGAATTTGTGTTT	3147

```

RESULT 11
US-10-211-179-11/c
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRESSION
; FILE REFERENCE: PTS-0011
; CURRENT APPLICATION NUMBER: US/10/211,179
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 119
; OTHER INFORMATION: n = a, t, c, or g
US-10-211-179-11

Query Match          11.0%; Score 89.4; DB 17; Length 158001;
Best Local Similarity 49.2%; Pred. No. 0.017;
Matches 265; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY      193 ATTAATGTTATTGGGACTTAACTAATTCTAGATATTAATTGTGGTTTGGAAGTTAATAATA 252
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      22732 ATAATATTATATATTAATTAATTAATATATATATTTTAAATTAATTAATTAATTAAT 22673

QY      253 ATTATTCATCCCTTGTTTTTATTTTTTTTATTAACAACAATTACCAATAATTATTTAA 312
        || | || | || | || | || | || | || | || | || | || | || | || | || |
DB      22672 ATATATTGTATATTTTTTTAATATATTATATATTTTAAATTAATTAATTAATTAAT 22613

QY      313 CTTTGGTTGTTTCCAATTATGACCGTTAATATTGTTTAAATTTGAGCATTTATAT 372
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      22612 TATATTTTATATATTTAATTAATAATATATATATTATTAATTTTATATATTATAATA 22553

QY      373 ATATTAATAATAATAATCAATGTAATATATGTAAAAATAATTTAAATATAAATTATTA 432
        ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      22552 ATATTAATAATAATTTAATAATTTAATAATA--ATAATAATTAATAATTTTATATAAT 22496

QY      433 ATATATATAATAACTCAATCAACAACAATAAAAAGATAAATAATTCTTAAATATATAAAT 492
        ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      22495 ATATATAATAATAATAATTTTATATATTTATATATTAATAATAATAATAATAATAAT 22436

QY      493 TTTTAAATAAGCTTTTGCTGAATCTGTCAACAACAATGAAAAATATTTTTTGACAGTTCAAT 552
        ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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D b	22435	ATTATATATATAATATATATATATTTTATATATTTATATATATATATATATATTT	22376
Q y	553	CCAAACACCAGAAAAGTAAATCAITTTTCAGAAAAGTAAATCAITTTTCAGAAATTAATTT	612
D b	22375	TTATATATTTTATATATATAATATATATATATATATATATTTTATATATATATAATATATAT	22316
Q y	613	TCGGAATTTATTTTACTGGCAACAATGGAGTCTAGTGTTCTGTTTATTTTATTTTAT	672
D b	22315	TATATATTTTATATATATTTTATATATATATATATATATATTTTATATATTTTATATATAT	22256
Q y	673	TTTTCTATTTAGAGAACTAGAAATTCATTTGTCAAATGCTTTAATCTAGCTTGTTTA	731
D b	22255	TTTTTATATTTATATATTTATATATATATTTACAATTTATATATAATATTTAATATATATTTATATA	22197

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RESULT 12
US-10-021-323-11125
; Sequence 11125, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 11125
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-034-Q6-N6-B10
US-10-021-323-11125

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Query Match	10.9%;	Score 89.2;	DB 17,	Length 565;
Best Local Similarity	51.5%;	Pred. No. 0.0038;		
Matches 205;	Conservative	0;	Mismatches 193;	Indels 0;
			Gaps	0
QY	194	TTAATGTTATTGGGATTACTAATTTCTAGTATTAATGTGGTTGGAGTTAATATATAA	253	
Db	2	TT	61	
QY	254	TTAATTCATCCTGGTTTTTTTATTTTTTTTTTATTAACACAATTAACAATTAATTTAAC	313	
Db	62	TT	121	
QY	314	TTTGGTTGTTTTCATTTATGACGGTTAATATTTTAGTTTAAATATGAGCATTTATTA	373	
Db	122	TT	181	
QY	374	TATTAATAATAATAATCATTTGTAATATATGTAATAAATAATTTTAAAAATTAATTA	433	
Db	182	AATTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAGGGAATAAAAAAAAAAAAAA	241	
QY	434	TATATATAATAACTCAATCAACAATAAAGATTAATAATTTCTAATAATATAATAATT	493	
Db	242	AAAG	301	
QY	494	TTTAAAAATAGCTTTTCAGTAATCTGTCAACAATAGAAATATTTTTGGCAGTTTCATC	553	
Db	302	AAAAAAATTTTTTAAAAAATAAAAAAAAAAAGAGGTTTAAAAAATTTTAA	361	
QY	554	CAAAACACGAAAAAGTAAATCATTTTCAGAAAAAGTAA	591	
Db	362	AAAAAGGGGAAAAAATAATTAATAAAAAAAAAAAAAA	399	

